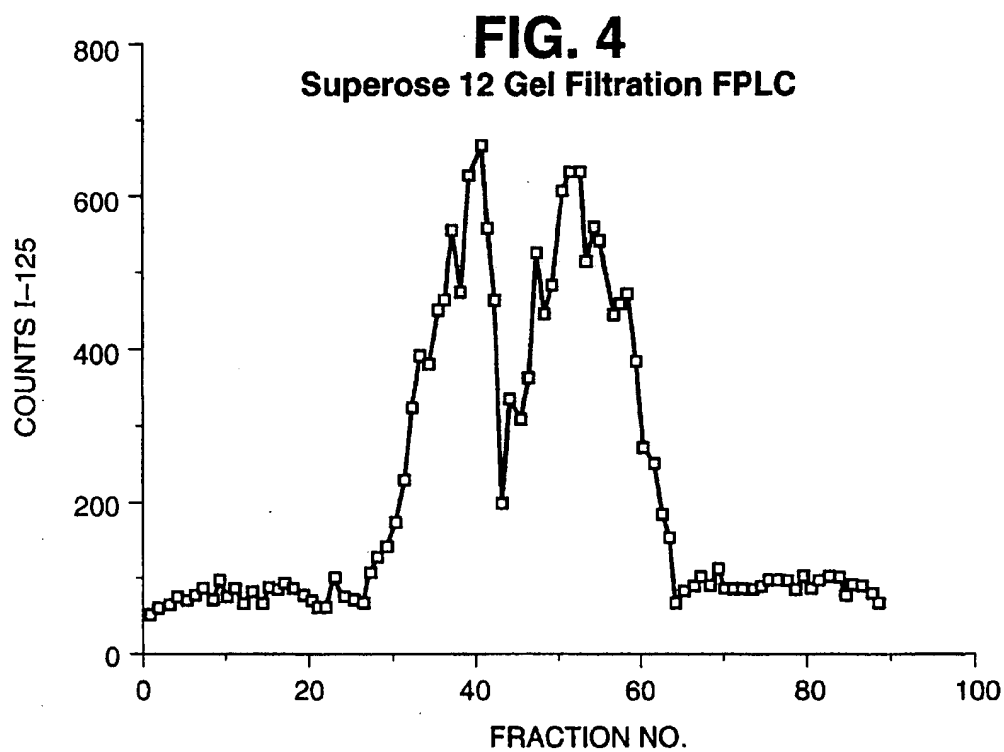
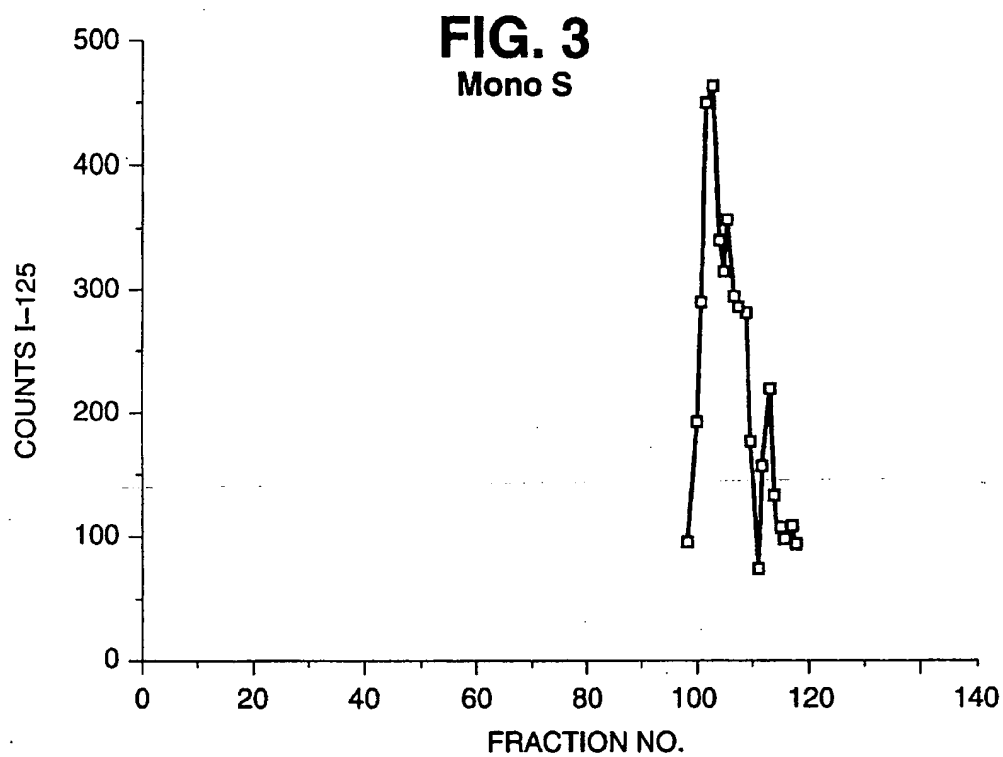
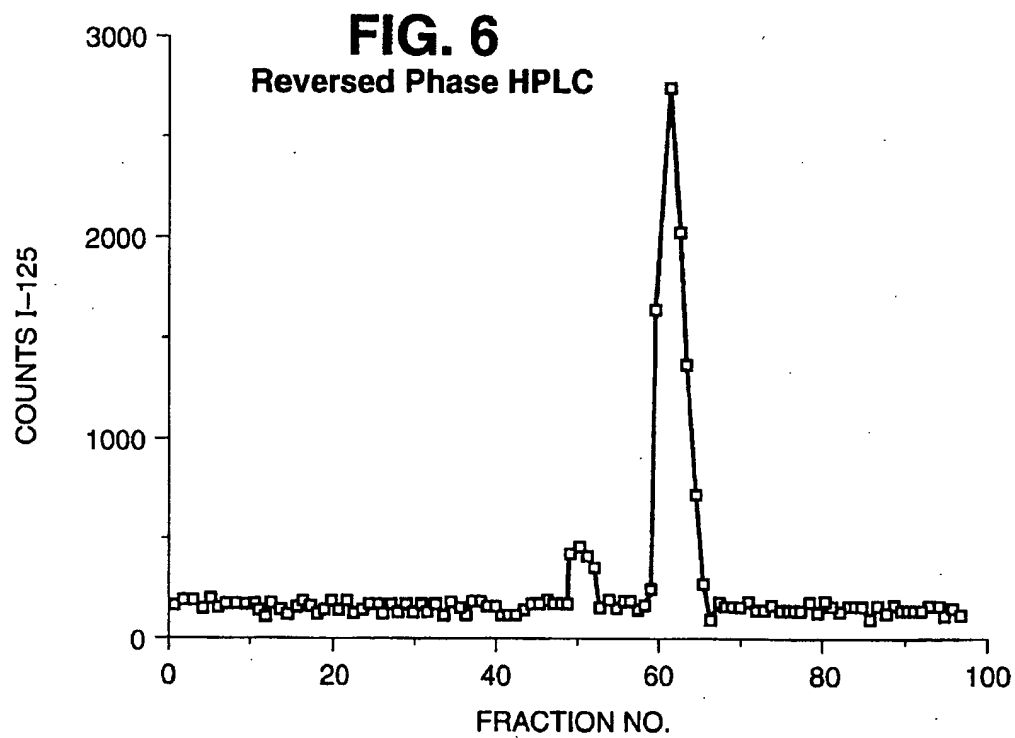
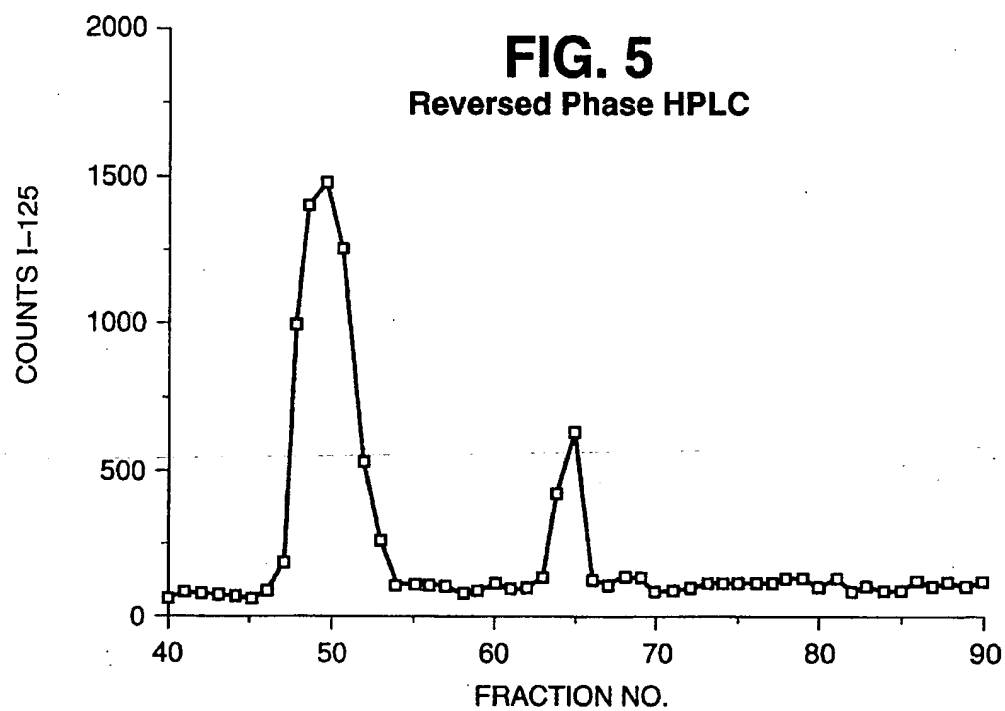


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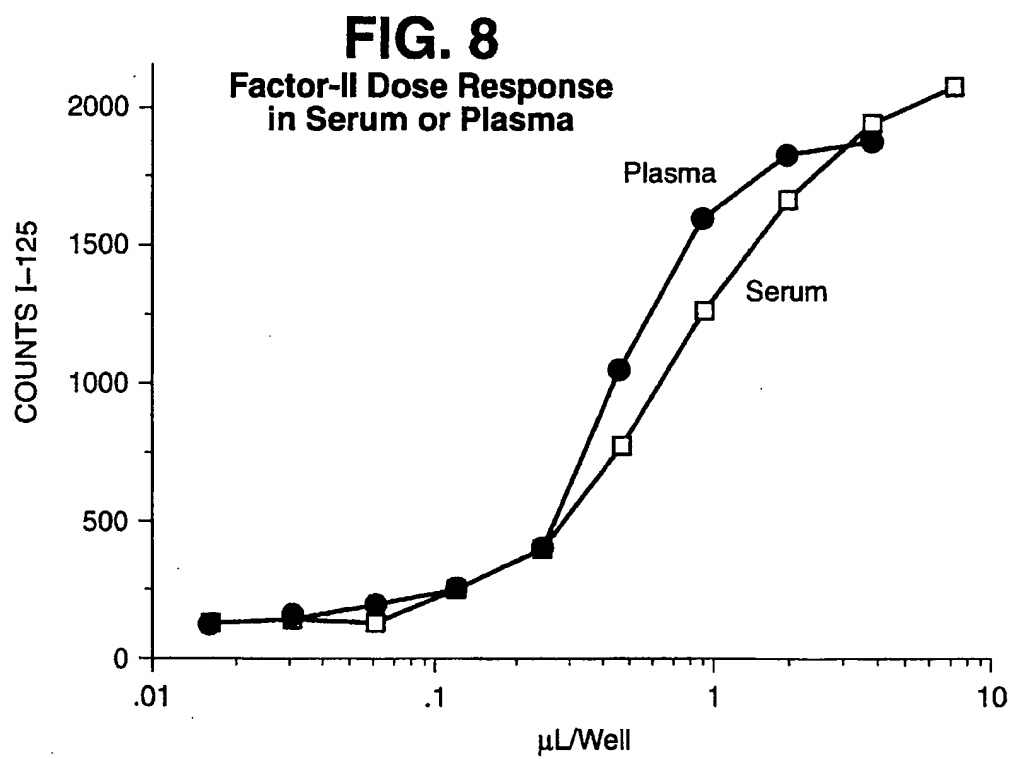
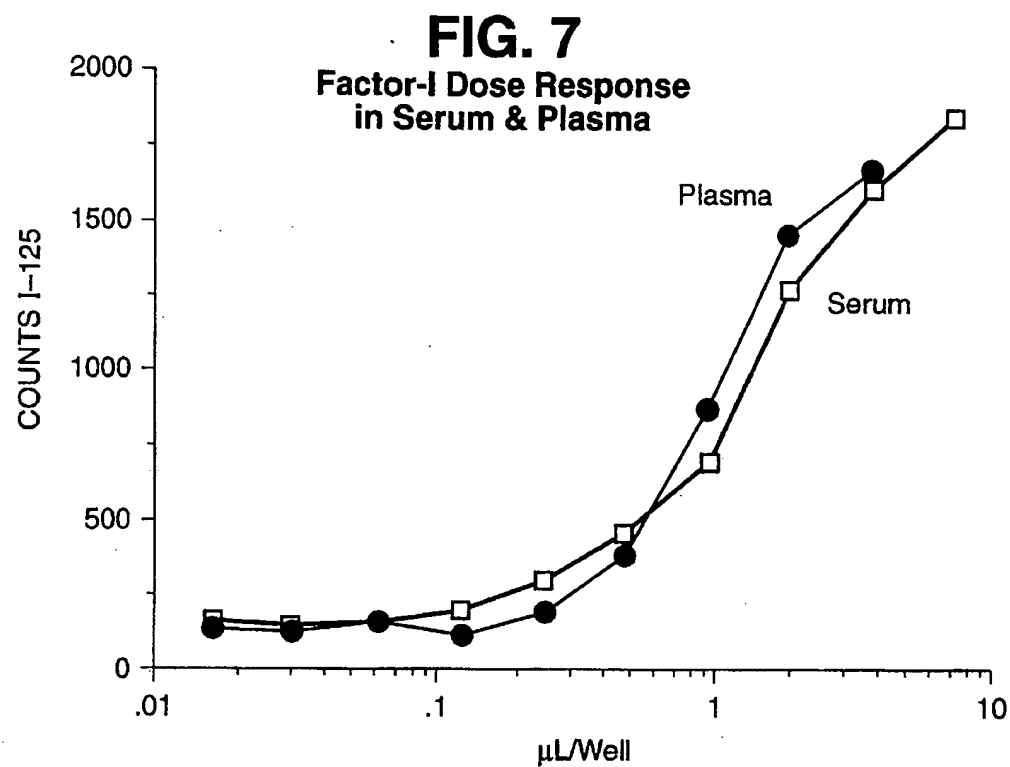


FIG. 9

| | | | |
|----------|---|------------------|----------|
| GGF-I 01 | N-terminus F K G D A H T E | (SEQ ID NO: 1) | |
| GGF-I 02 | Trypsin peptides K/R A S L A D E Y E Y M X K * | (SEQ ID NO: 2) | |
| GGF-I 03 | K/R T E T S S G L X L K * | (SEQ ID NO: 3) | |
| GGF-I 04 | K/R K L G E M W A E | (SEQ ID NO: 4) | HMG-1 |
| GGF-I 05 | K/R L G E K R A | (SEQ ID NO: 5) | HMG-1? |
| GGF-I 06 | K/R I K S E H A G L S I G D T A K * | (SEQ ID NO: 6) | HMG-2 |
| GGF-I 07 | K/R A S L A D E Y E Y M R K * | (SEQ ID NO: 7) | |
| GGF-I 08 | K/R I K G E H P G L S I G D V A K * | (SEQ ID NO: 8) | HMG-1 |
| GGF-I 09 | K/R M S E Y A F F V Q T X R * | (SEQ ID NO: 9) | HMG-2 |
| GGF-I 10 | K/R S E H P G L S I G D T A K * | (SEQ ID NO: 10) | HMG-1 |
| GGF-I 11 | K/R A G Y F A E X A R * | (SEQ ID NO: 11) | |
| GGF-I 12 | K/R K L E F L X A K * | (SEQ ID NO: 12) | |
| GGF-I 13 | K/R T T E M A S E Q G A | (SEQ ID NO: 13) | |
| GGF-I 14 | K/R A K E A L A A L K * | (SEQ ID NO: 14) | |
| GGF-I 15 | K/R F V L Q A K K * | (SEQ ID NO: 15) | |
| GGF-I 16 | K/R L G E M W | (SEQ ID NO: 16) | HMG-1 |
| GGF-I 17 | Protease V8 peptides E T Q P D P G Q I L K K V P M V I G A Y T | (SEQ ID NO: 169) | |
| GGF-I 18 | E Y K C L K F K W F K K A T V M | (SEQ ID NO: 17) | |
| GGF-I 19 | E A K Y F S K X D A | (SEQ ID NO: 18) | LH-alpha |
| GGF-I 20 | E X K F Y V P | (SEQ ID NO: 19) | |
| GGF-I 21 | E L S F A S V R L P G C P P G V D P M V S F P V A L | (SEQ ID NO: 20) | LH-beta |

FIG. 10

A

| | | |
|----------|---|-----------------|
| GGF-I 01 | F K G D A H T E | (SEQ ID NO: 1) |
| GGF-I 02 | A S L A D E Y E Y M X K | (SEQ ID NO: 22) |
| GGF-I 03 | T E T S S G L X L K | (SEQ ID NO: 23) |
| GGF-I 07 | A S L A D E Y E Y M R K | (SEQ ID NO: 24) |
| GGF-I 11 | A G Y F A E X A R | (SEQ ID NO: 25) |
| GGF-I 13 | T T E M A S E Q G A | (SEQ ID NO: 26) |
| GGF-I 14 | A K E A L A L K | (SEQ ID NO: 27) |
| GGF-I 15 | F V L Q A K K | (SEQ ID NO: 28) |
| GGF-I 17 | E T Q P D P G Q I L K K V P M V I G A Y T | (SEQ ID NO: 29) |
| GGF-I 18 | E Y K C L K F K W F K K A T V M | (SEQ ID NO: 17) |

B

| | | |
|----------|-----------------|-----------------|
| GGF-I 20 | E X K F Y V P | (SEQ ID NO: 19) |
| GGF-I 12 | K L E F L X A K | (SEQ ID NO: 32) |

[illegible]

FIG. 12

A

| | | |
|-----------|-------------------------------|-----------------|
| GGF-II 01 | V H Q V W A A K | (SEQ ID NO: 45) |
| GGF-II 02 | Y I F M E P E A X S S G | (SEQ ID NO: 46) |
| GGF-II 03 | L G A W G P P A F P V X Y | (SEQ ID NO: 47) |
| GGF-II 04 | W F V V I E G K | (SEQ ID NO: 48) |
| GGF-II 08 | A S P V S V G S V Q E L V Q R | (SEQ ID NO: 49) |
| GGF-II 09 | V C L L T V A A P P T | (SEQ ID NO: 50) |
| GGF-II 11 | K V H Q V W A A K | (SEQ ID NO: 51) |
| GGF-II 12 | K A S L A D S G E Y M X K | (SEQ ID NO: 52) |

B

Novel Factor II Peptides - others

| | | |
|-----------|-------------|-----------------|
| GGF-II 10 | D L L L X V | (SEQ ID NO: 53) |
|-----------|-------------|-----------------|

FIG. 13

Comparison of BrdU-ELISA and [125 I]UdR Counting Method for the DNA Synthesis Assay in Schwann Cell Cultures

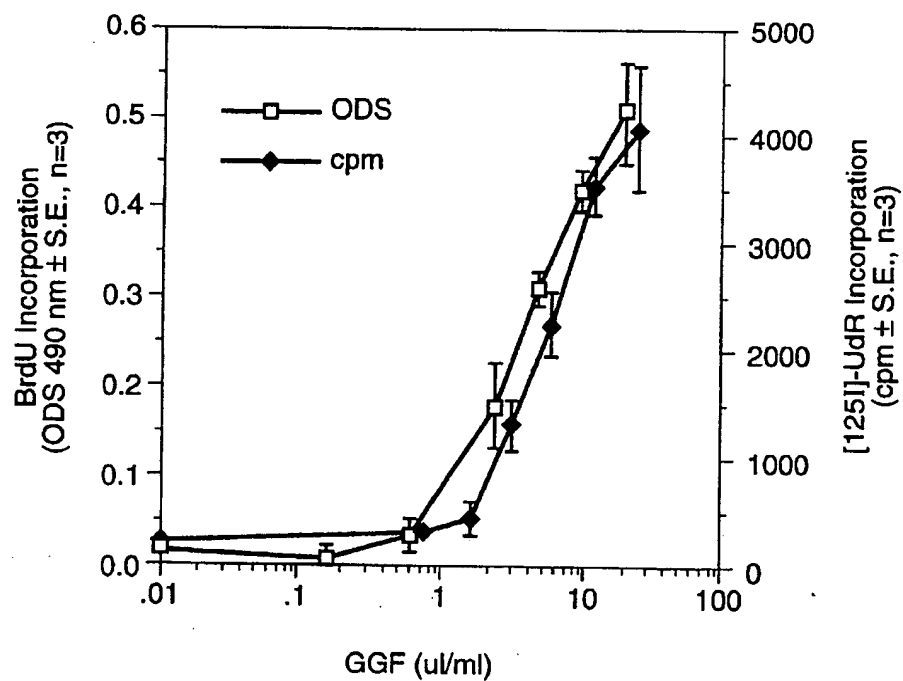


FIG. 14A

**Comparison of Br-UdR Immunoreactivity
and Br-UdR Labelled Cell Number**

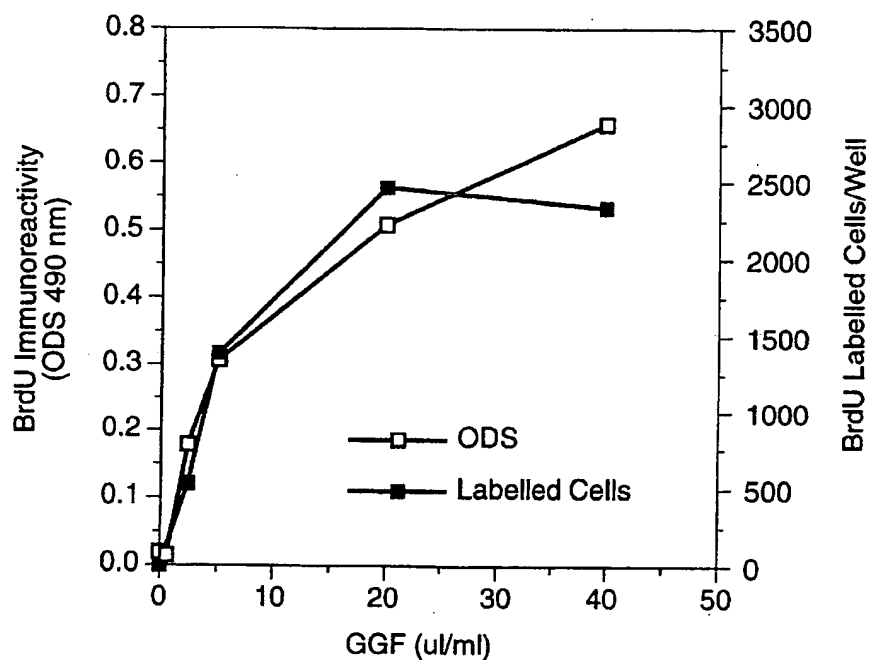


FIG. 14B

**Comparison of Br-UdR Immunoreactivity
and Br-UdR Labelled Cell Number**

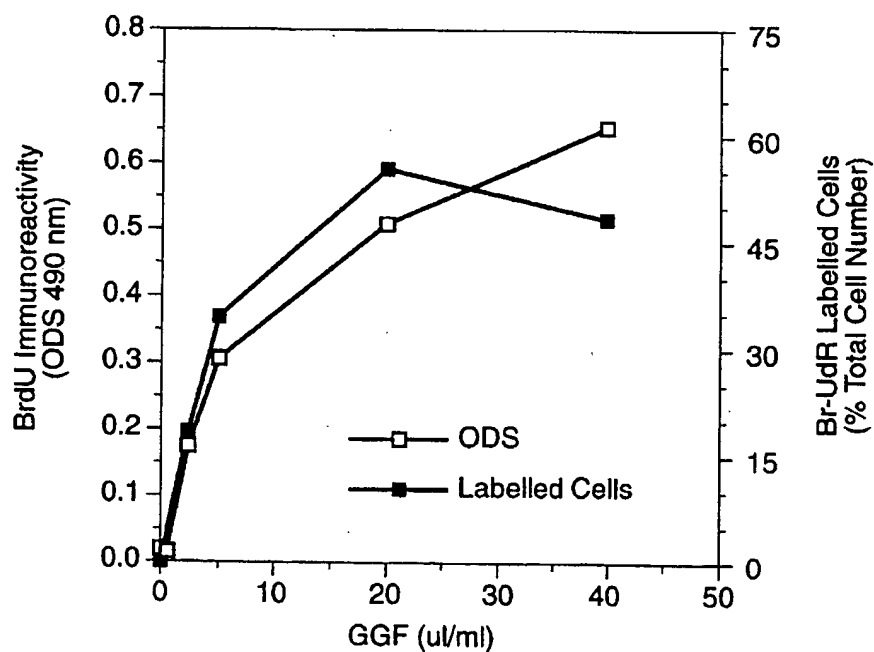


FIG. 15

Mitogenic Response of Rat Sciatic Nerve Schwann cell to GGFs

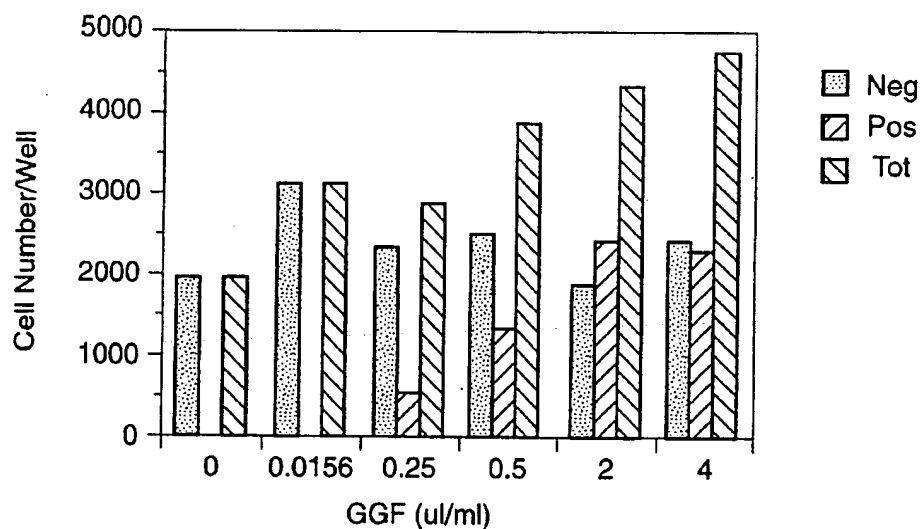


FIG. 16

DNA Synthesis in Rat Sciatic Nerve Schwann Cells and 3T3 Fibroblasts in the presence of GGFs

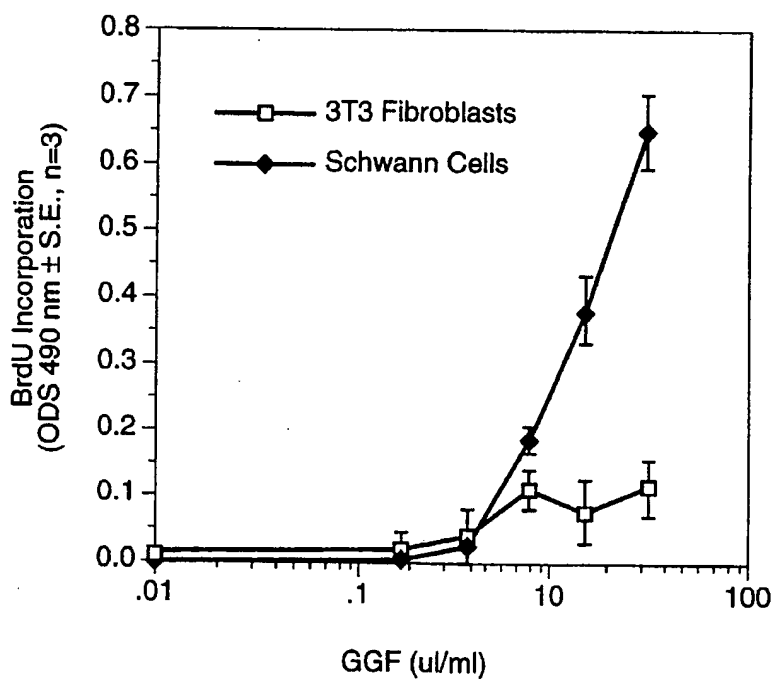


FIG. 17
Mitogenic Response of
BHK 21 C13 Cells to FCS and GGFs

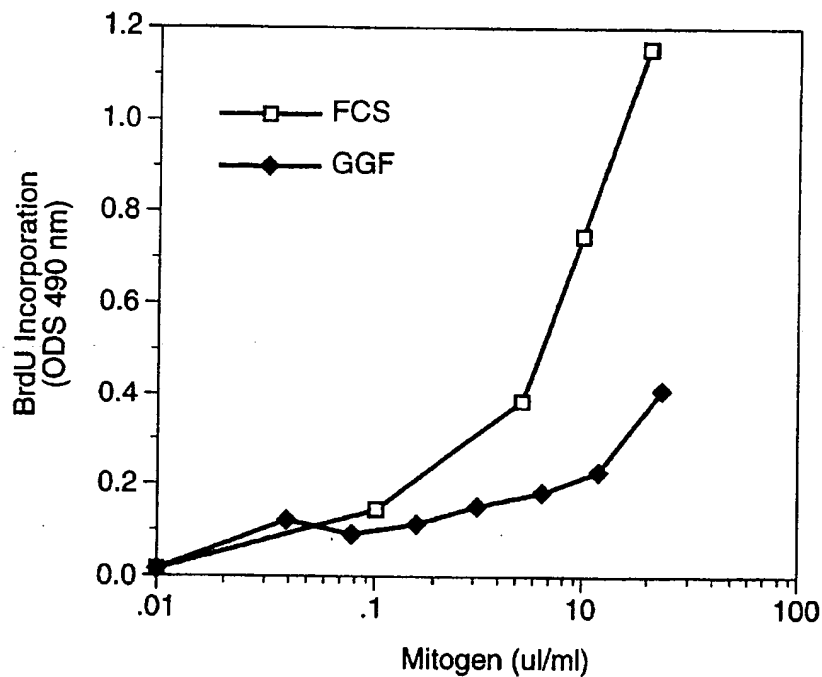


FIG. 18
Survival and Proliferation of BHK21 C13 Cell
Microcultures After 48 Hours in Presence of GGFs

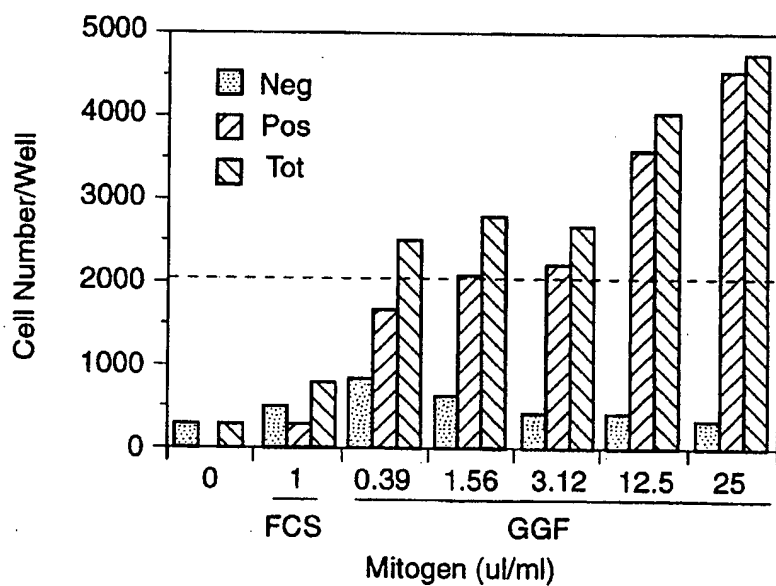


FIG. 19
Mitogenic Response
of C6 Cells to FCS

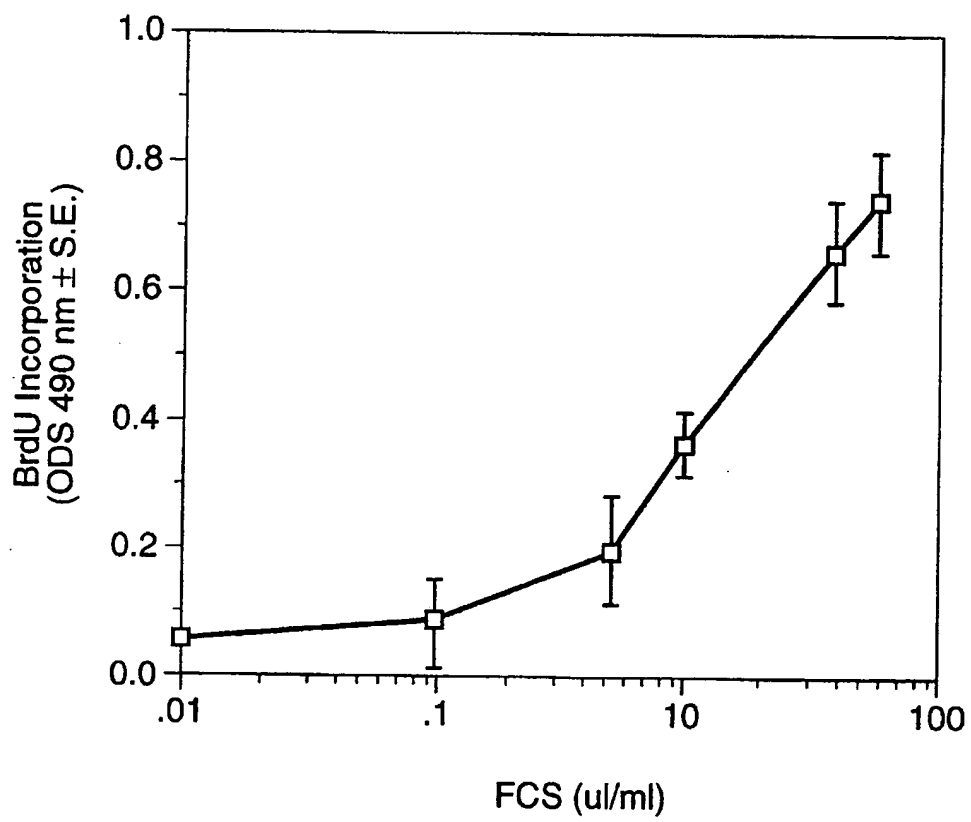


FIG. 20A
Mitogenic Response of
C6 Cells to aFGF & GGFS

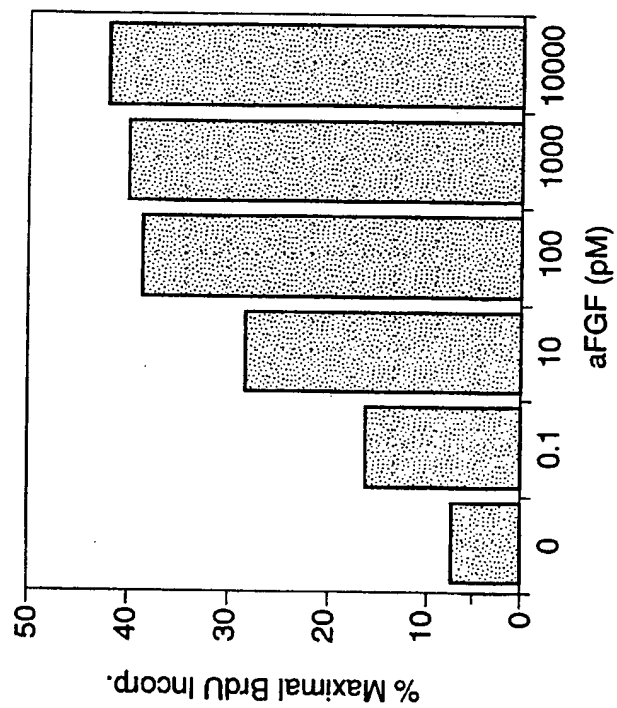


FIG. 20B
Mitogenic Response of
C6 Cells to aFGF & GGFS

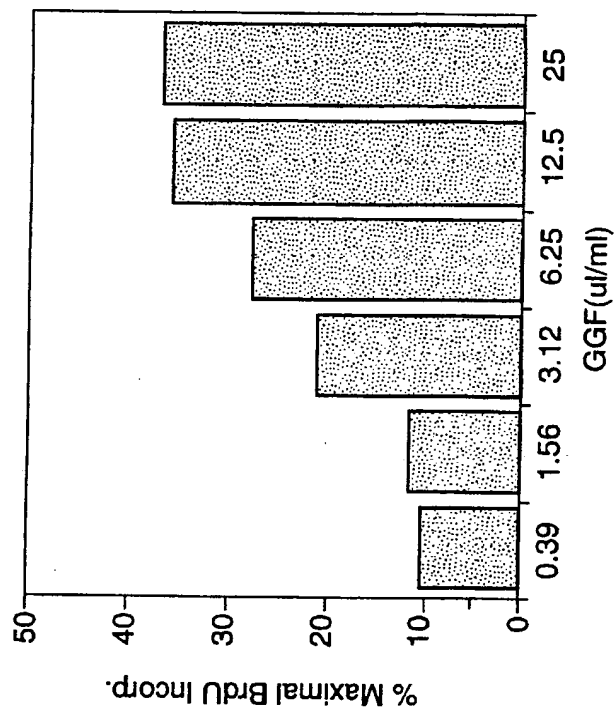


FIG. 21

Degenerate Oligonucleotide Probes for Factor I & Factor II

| Oligo | Sequence | Peptide | |
|-------|-------------------------|----------|-----------------|
| 535 | TTYAARGGNGAYGCNCAYAC! | GGFI-1 | (SEQ ID NO: 54) |
| 536 | CATRTAYTCRTAYTCRTCNGC! | GGFI-2 | (SEQ ID NO: 55) |
| 537 | TGYTCNGANGCCATYTCNGT! | GGFI-13 | (SEQ ID NO: 56) |
| 538 | TGYTCRCTNGCCATYTCNGT! | GGFI-13 | (SEQ ID NO: 57) |
| 539 | CCDATNACCATNGGNACYTT! | GGFI-17 | (SEQ ID NO: 58) |
| 540 | GCNGCCCANACYTGRTGNAC! | GGFII-1 | (SEQ ID NO: 59) |
| 541 | GCYTCNGGYYTCCATRAARAA! | GGFII-2 | (SEQ ID NO: 60) |
| 542 | CCYTCDATNACNACRAACCA! | GGFII-4 | (SEQ ID NO: 61) |
| 543 | TCNGCRAARTANCCNGC! | GGFI-11 | (SEQ ID NO: 62) |
| 544 | GCNGCNAGNGCYTCYTTNGC! | GGFI-14 | (SEQ ID NO: 63) |
| 545 | GCNGCYAANGCYTCYTTNGC! | GGFI-14 | (SEQ ID NO: 64) |
| 546 | TTYTTNGCYTGNAGNACRAA! | GGFI-15 | (SEQ ID NO: 65) |
| 551 | TTYTTNGCYTGYAANACRAA! | GGFI-15 | (SEQ ID NO: 66) |
| 568 | TGNACNAGYTCYTGNAC! | GGFII-8 | (SEQ ID NO: 67) |
| 569 | TGNACYAAAYTCYTGNAC! | GGFII-8 | (SEQ ID NO: 68) |
| 609 | CATRTAYTCNCCNGARTCNGC! | GGFII-12 | (SEQ ID NO: 69) |
| 610 | CATRTAYTCNCCRCTRRTCNGC! | GGFII-12 | (SEQ ID NO: 70) |
| 649 | NGARTCNGCYAANGANGCYTT! | GGFII-12 | (SEQ ID NO: 71) |
| 650 | NGARTCNGCNAGNGANGCYTT! | GGFII-12 | (SEQ ID NO: 72) |
| 651 | RCTRRTCNGCYAANGANGCYTT! | GGFII-12 | (SEQ ID NO: 73) |
| 652 | RCTRRTCNGCNAGNGANGCYTT! | GGFII-12 | (SEQ ID NO: 74) |
| 653 | NGARTCNGCYAARCTNGCYTT! | GGFII-12 | (SEQ ID NO: 75) |
| 654 | NGARTCNGCNAGRCTNGCYTT! | GGFII-12 | (SEQ ID NO: 76) |
| 655 | RCTRRTCNGCYAARCTNGCYTT! | GGFII-12 | (SEQ ID NO: 78) |
| 656 | RCTRCTNGCNAGRCTNGCYTT! | GGFII-12 | (SEQ ID NO: 79) |
| 659 | ACNACNGARATGGCTCNNGA! | GGFI-13 | (SEQ ID NO: 80) |
| 660 | ACNACNGARATGGCAGYNGA! | GGFI-13 | (SEQ ID NO: 81) |
| 661 | CAYCARGTNTGGGCNGCNAA! | GGFII-1 | (SEQ ID NO: 82) |
| 662 | TTYGTNGTNATHGARGGNAA! | GGFII-4 | (SEQ ID NO: 83) |
| 663 | AARGGNGAYGCNCAYACNGA! | GGFI-1 | (SEQ ID NO: 84) |
| 664 | GARGCNYTNGCNGCNYTNAA! | GGDI-14 | (SEQ ID NO: 85) |
| 665 | GTNGGNTCNGTNCARGARYT! | GGFII-8 | (SEQ ID NO: 86) |
| 666 | GTNGGNAGYGTNCARGARYT! | GGFII-8 | (SEQ ID NO: 87) |
| 694 | NACYTTYTTNARHATYTGNC! | GGFI-17 | (SEQ ID NO: 88) |

FIG. 22

Putative Bovine Factor II Gene Sequences

SEQ ID NO: 89:

| | |
|--|-----|
| TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile | 53 |
| CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile | 101 |
| AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile | 149 |
| AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu | 197 |
| TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA Ser Asn Gly Lys Arg Cys Leu Arg Ala Ile Ser Gln Ser Leu Arg | 245 |
| GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu | 293 |
| ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu | 341 |
| AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu | 389 |
| ATA GAC CTG AAA TAT ATA TAG ATT ATT T Ile Asp Leu Lys Tyr Ile Xaa Ile Ile | 417 |

FIG. 23A

PCR Primers for Factor I & Factor II

Degenerate PCR Primers

| Oligo Sequence | Peptide | (SEQ ID NO: 90) |
|---|---------|------------------|
| 657 CCGAATTCTGCAGGARACNCARCCNGAYCCNNGG! | GGFI-17 | (SEQ ID NO: 91) |
| 658 AAGGATCCTGCAGNGTRTANGCNCCHATNACCATNNGG! | GGFI-17 | (SEQ ID NO: 92) |
| 667 CCGAATTCTGCAGGCNGAYTCNCGNGARTAYATG! | GGFI-12 | (SEQ ID NO: 93) |
| 668 CCGAATTCTGCAGGCNGAYATYGGNGARTAYAT! | GGFI-12 | (SEQ ID NO: 94) |
| 669 AAGGATCCTGCAGNNNCATRTAYTCNCCNGARTC! | GGFI-12 | (SEQ ID NO: 95) |
| 670 AAGGATCCTGCAGNNNCATRTAYTCNCCRRTRTC! | GGFI-12 | (SEQ ID NO: 96) |
| 671 CCGAATTCTGCAGCAYCARGTNTGGCNGCNAA! | GGFI-1 | (SEQ ID NO: 97) |
| 672 CCGAATTCTGCAGATRTTYTTYATGGARCCNGARG! | GGFI-2 | (SEQ ID NO: 98) |
| 673 CCGAATTCTGCAGGGGNCNCNCNTTYCCNGT! | GGFI-3 | (SEQ ID NO: 99) |
| 674 CCGAATTCTGCAGTGGTTYGTNGTNAATHGARGG! | GGFI-4 | (SEQ ID NO: 100) |
| 677 AAGGATCCTGCAGYTTNGCNGCCCCANACYTGRTG! | GGFI-1 | (SEQ ID NO: 101) |
| 678 AAGGATCCTGCAGGCYTCNGGYTCCATRAARAA! | GGFI-2 | (SEQ ID NO: 102) |
| 679 AAGGATCCTGCAGACNGGGAANGCNGGNGNCC! | GGFI-3 | (SEQ ID NO: 103) |
| 680 AAGGATCCTGCAGYTTNCCYTCDATNACNACRAAC! | GGFI-4 | (SEQ ID NO: 104) |
| 681 CATRTAYTCRTAYTCTCNGCAAGGATCCTGCAG! | GGFI-2 | (SEQ ID NO: 105) |
| 682 CCGAATTCTGCAGAAARGNGAYGCNCAYACNGA! | GGFI-1 | (SEQ ID NO: 106) |
| 683 GCNGCYAANGCYRCYTTNGCAAGGATCCTGCAG! | GGFI-14 | (SEQ ID NO: 107) |
| 684 GCNGCNAGNGCYTCYTTNGCAAGGATCCTGCAG! | GGFI-14 | (SEQ ID NO: 108) |
| 685 TCNGCRAARTANCCNGCAAGGATCCTGCAG! | GGFI-1 | |

FIG. 23B **PCR Primers for Factor I & Factor II**

Unique PCR Primers for Factor II

| Oligo Sequence | Comment | (SEQ ID NO: 109) |
|---|-------------------|------------------|
| 711 CATCGATCTGCAGGCTGATTCTGGAGAAATATATGTGCA! | 3' RACE | (SEQ ID NO: 110) |
| 712 AAGGATCCTGCAGCCACATCTCGAGTCGACATCGATT! | 3' RACE | (SEQ ID NO: 111) |
| 713 CCGAATTCTGCAGTGATCAGCAAACTAGGAAATGACA! | 3' RACE | (SEQ ID NO: 112) |
| 721 CATCGATCTGCAGCCTAGTTTGCTGATCACTTTGCAC! | 5' RACE | (SEQ ID NO: 113) |
| 722 AAGGATCCTGCAGTATATTCTCCAGAATCAGCCAGTG! | 5' RACE; ANCHORED | (SEQ ID NO: 114) |
| 725 AAGGATCCTGCAGGCACGACGTAGGCATCTCTTA! | EXON A | (SEQ ID NO: 115) |
| 726 CCGAATTCTGCAGCAGAACTTCGCATTAGCAAAGC! | EXON A | (SEQ ID NO: 116) |
| 771 CATCCCGGGATGAAGAGTCAGGAGTCTGTGGCA! | EXONS B+A | (SEQ ID NO: 117) |
| 772 ATACCCGGGCTGCAGACAAATGAGATTTCACACACCTGCG! | | (SEQ ID NO: 118) |
| 773 AAGGATCCTGCAGTTTGGAACCTGCCACAGACTCCT! | ANCHORED | (SEQ ID NO: 119) |
| 776 ATACCCGGGCTGCAGATGAGATTTCACACACCTGCGTGA! | EXONS B+A | |

FIG. 24
Summary of Contiguous GGF-II
cDNA Structures & Sequences

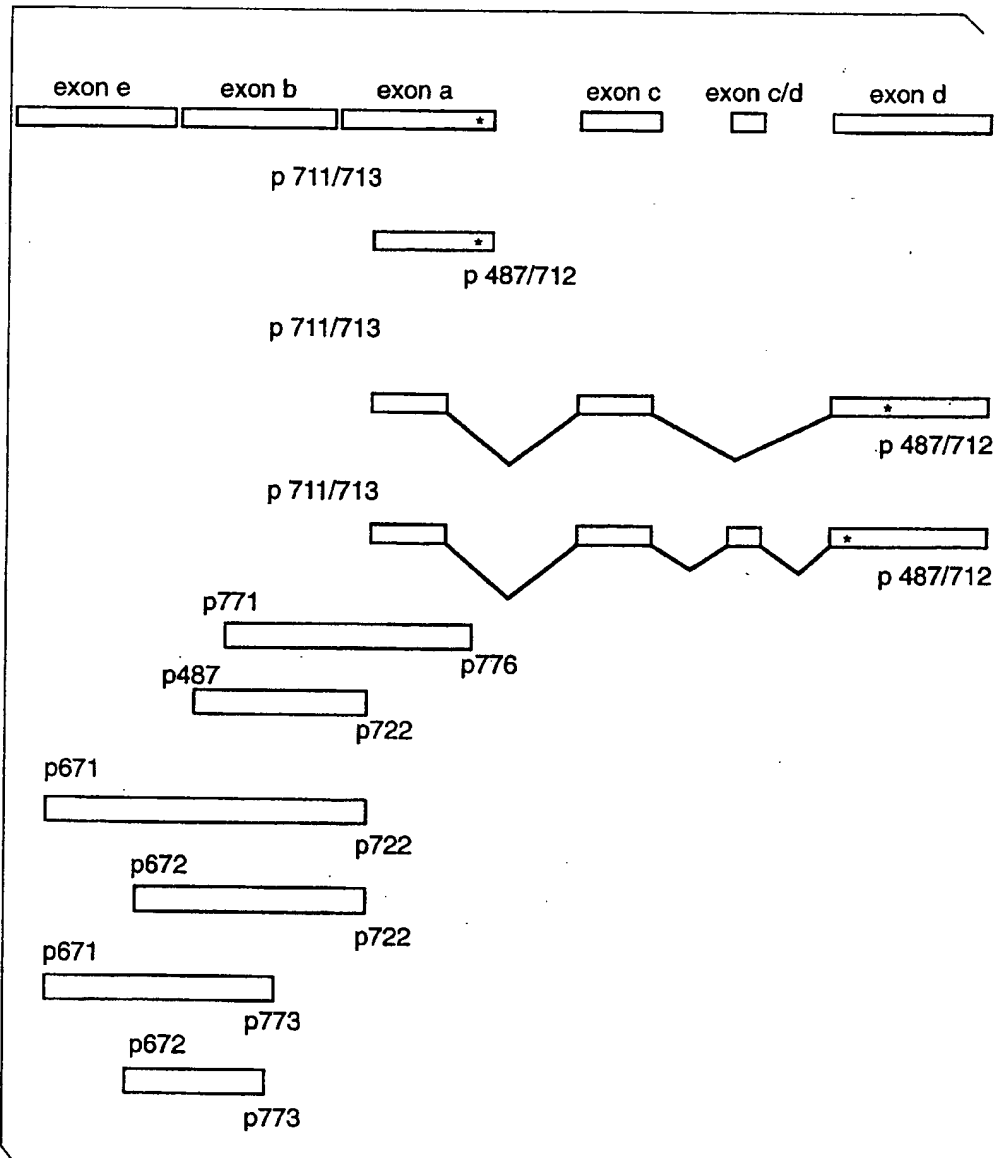


FIG. 25

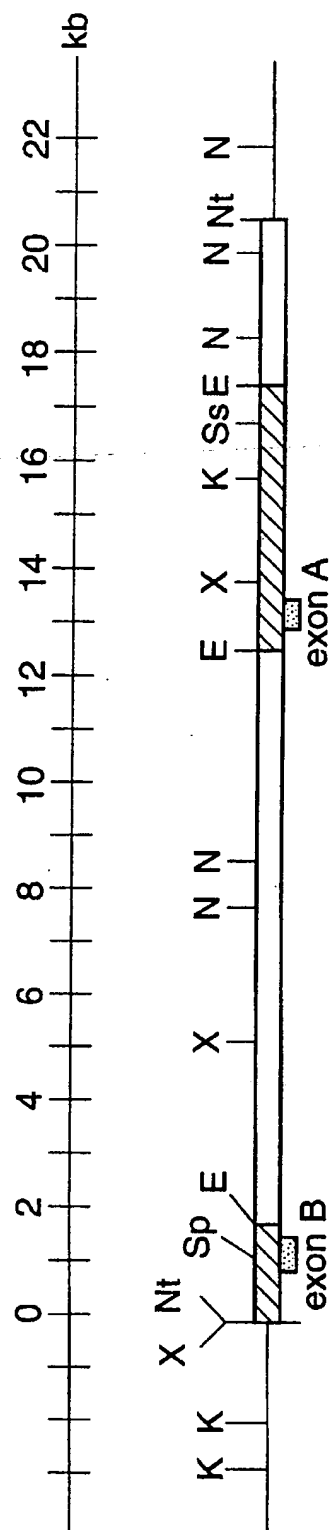


FIG. 26
Alternative Gene Products of Putative Bovine GGF-II

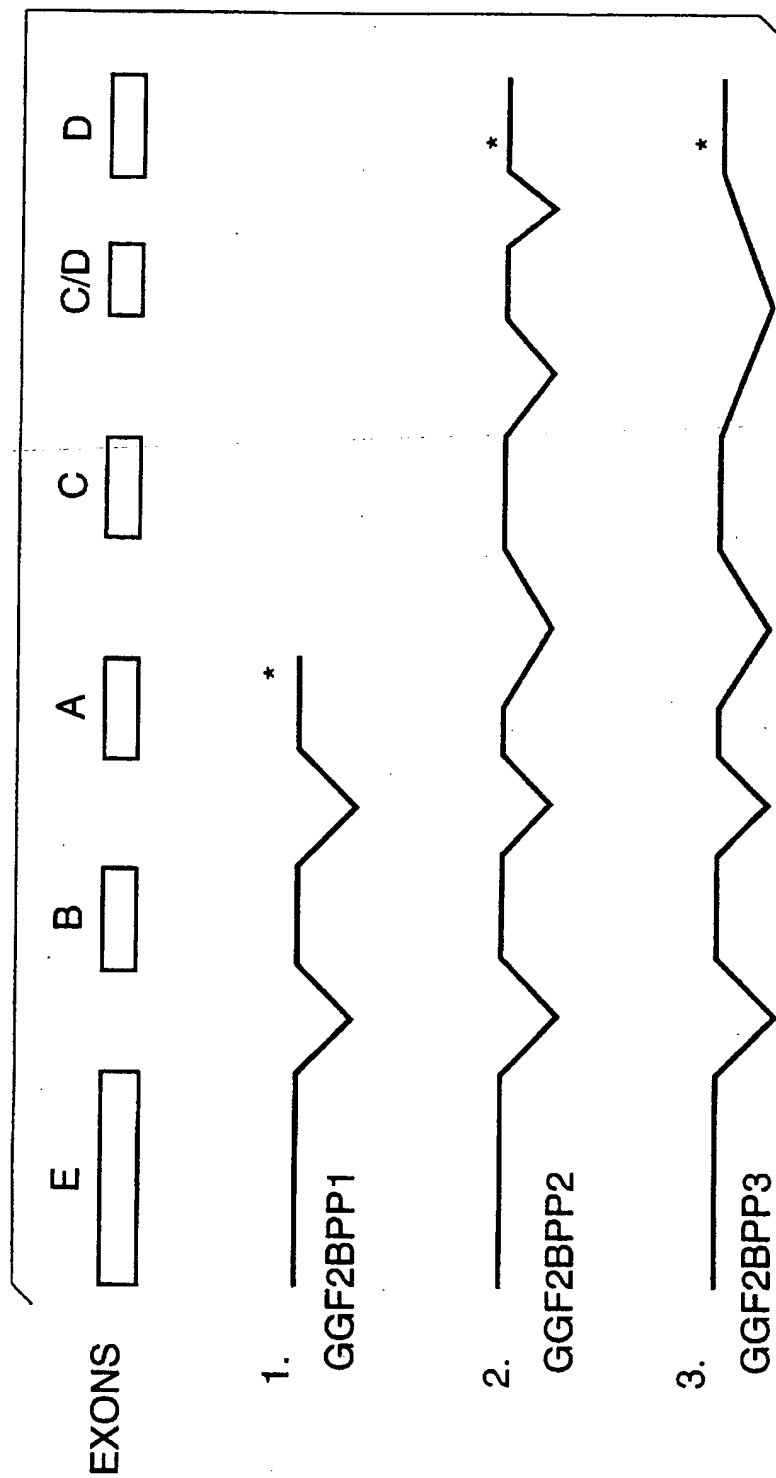


FIG. 27

GGF-II Peptides Identified in Deduced Amino Acid Sequences of Putative Bovine GGF-II Proteins

| Peptide | Pos. | Sequence match | ID Sequences |
|---------|------|--|------------------------------------|
| II-1 | 1: | VHQVWAAK HQVWAAK AAGLK | (SEQ ID NO:120) |
| II-10 | 14: | DLLLXV GGLKK dslltv RLGAW | (SEQ ID NO:121) |
| II-03 | 21: | LGAWGPPAFPVXY LLTVR lgawghpafpvcg RLKED | (SEQ ID NO:122) (SEQ ID NO:123) |
| II-02 | 41: | YIFFMEPEAXSSG KEDSR YIFFMEPEANSSG GPGRL | (SEQ ID NO:124) (SEQ ID NO:125) |
| II-6 | 103: | LVLRL VAGSK LVLRL CETSS | (SEQ ID NO:126) |
| I-18 | 112: | EYKCLKFKWFKKATVM CETSS eysslkfkfwkngsel SRKNK | (SEQ ID NO:127) (SEQ ID NO:128) |
| II-12 | 151: | KASLADSGEYMXK ELRIS KASLADSGEYMCK VISKL | (SEQ ID NO:129) (SEQ ID NO:130) |
| I-07 | 152: | ASLADEYEYMRK LRISK asladsgeymck VISKL | (SEQ ID NO:131) (SEQ ID NO:132) |

FIG. 28A

SEQ ID NO: 133:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Ser Leu

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GGC TTC CCC TCC TGC 103
Leu Thr Val Arg Leu Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 151
Gly Arg Leu Lys Gln Asp Ser Arg Tyr Ile Phe Phe Met Gln Pro Glu

GCC AAC AGC AGC GGC GGC CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC 199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn

ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT 583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile

TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT 625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr

TGAATCACGC AGGTGTGTGA AATCTCATTTG TGAACAATA AATATCATGA AAGGAAAAA 685
AAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC 744

FIG. 28B

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP2

SEQ ID NO: 134:

| | | | | | | | | | | | | | | | | | |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CCTGCAG | CAT | CAA | GTG | TGG | GCG | GCG | AAA | GCC | GGG | GGC | TTG | AAG | AAG | GAC | TCG | CTG | 55 |
| | His | Gln | Val | Trp | Ala | Ala | Lys | Ala | Gly | Gly | Leu | Lys | Lys | Asp | Ser | Leu | |
| CTC | ACC | GTG | CGC | CTG | GGC | GCC | TGG | GGC | CAC | CCC | GCC | TTC | CCC | TCC | TGC | | 103 |
| Leu | Thr | Val | Arg | Leu | Gly | Ala | Trp | Gly | His | Pro | Ala | Phe | Pro | Ser | Cys | | |
| GGG | CGC | CTC | AAG | GAG | GAC | AGC | AGG | TAC | ATC | TTC | TTC | ATG | GAG | CCC | GAG | | 151 |
| Gly | Arg | Leu | Lys | Glu | Asp | Ser | Arg | Tyr | Ile | Phe | Phe | Met | Glu | Pro | Glu | | |
| GCC | AAC | AGC | AGC | GGC | GGG | CCC | GGC | CGC | CTT | CCG | AGC | CTC | CTT | CCC | CCC | | 199 |
| Ala | Lys | Ser | Ser | Gly | Gly | Pro | Gly | Arg | Leu | Pro | Ser | Leu | Leu | Pro | Pro | | |
| TCT | CGA | GAC | GGG | CCG | GAA | CCT | CAA | GAA | GGA | GGT | CAG | CCG | GGT | GCT | GTG | | 247 |
| Ser | Arg | Asp | Gly | Pro | Glu | Pro | Gln | Glu | Gly | Gly | Gln | Pro | Gly | Ala | Val | | |
| CAA | CGG | TGC | GCC | TTG | CCT | CCC | CGC | TTG | AAA | GAG | ATG | AAG | AGT | CAG | GAG | | 295 |
| Gln | Arg | Cys | Ala | Leu | Pro | Pro | Arg | Leu | Lys | Glu | Met | Lys | Ser | Gln | Glu | | |
| TCT | GTG | GCA | GGT | TCC | AAA | CTA | GTG | CTT | CGG | TGC | GAG | ACC | AGT | TCT | GAA | | 343 |
| Ser | Val | Ala | Gly | Ser | Lys | Leu | Val | Leu | Arg | Cys | Glu | Thr | Ser | Ser | Glu | | |
| TAC | TCC | TCT | CTC | AAG | TTC | AAG | TGG | TTC | AAG | AAT | GGG | AGT | GAA | TTA | AGC | | 391 |
| Tyr | Ser | Ser | Leu | Lys | Phe | Lys | Trp | Phe | Lys | Asn | Gly | Ser | Glu | Leu | Ser | | |
| CGA | AAG | AAC | AAA | CCA | GAA | AAC | ATC | AAG | ATA | CAG | AAA | AGG | CCG | GGG | AAG | | 439 |
| Arg | Lys | Asn | Lys | Gly | Gly | Asn | Ile | Lys | Ile | Gln | Lys | Arg | Pro | Gly | Lys | | |
| TCA | GAA | CTT | CGC | ATT | AGC | AAA | GCG | TCA | CTG | GCT | GAT | TCT | GGA | GAA | TAT | | 487 |
| Ser | Glu | Leu | Arg | Ile | Ser | Lys | Ala | Ser | Leu | Ala | Asp | Ser | Gly | Glu | Tyr | | |
| ATG | TGC | AAA | GTG | ATC | AGC | AAA | CTA | GGA | AAT | GAC | AGT | GCC | TCT | GCC | AAC | | 535 |
| Met | Cys | Lys | Lys | Val | Ile | Ser | Lys | Gly | Asn | Asp | Ser | Ala | Ser | Ala | Asn | | |

FIG. 28C

Nucleotide Sequences & Deduced Amino Acid Sequences of GG2BPP2

| | |
|--|------|
| ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr | 583 |
| AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn | 631 |
| GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr | 679 |
| TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn | 727 |
| GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu | 775 |
| GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC Val Ile Ala Ala Lys Thr Thr | 826 |
| CCTTTCTGTC TCTGCCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC | 886 |
| TCCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCCTCT | 946 |
| GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT | 1006 |
| GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGT TCTGAAATTG ATCTTGAATT | 1066 |
| ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA | 1126 |
| GTCAAAAAAA AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC | 1186 |
| TCTAGAG | 1193 |

FIG. 28D

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP3

SEQ ID NO: 135:

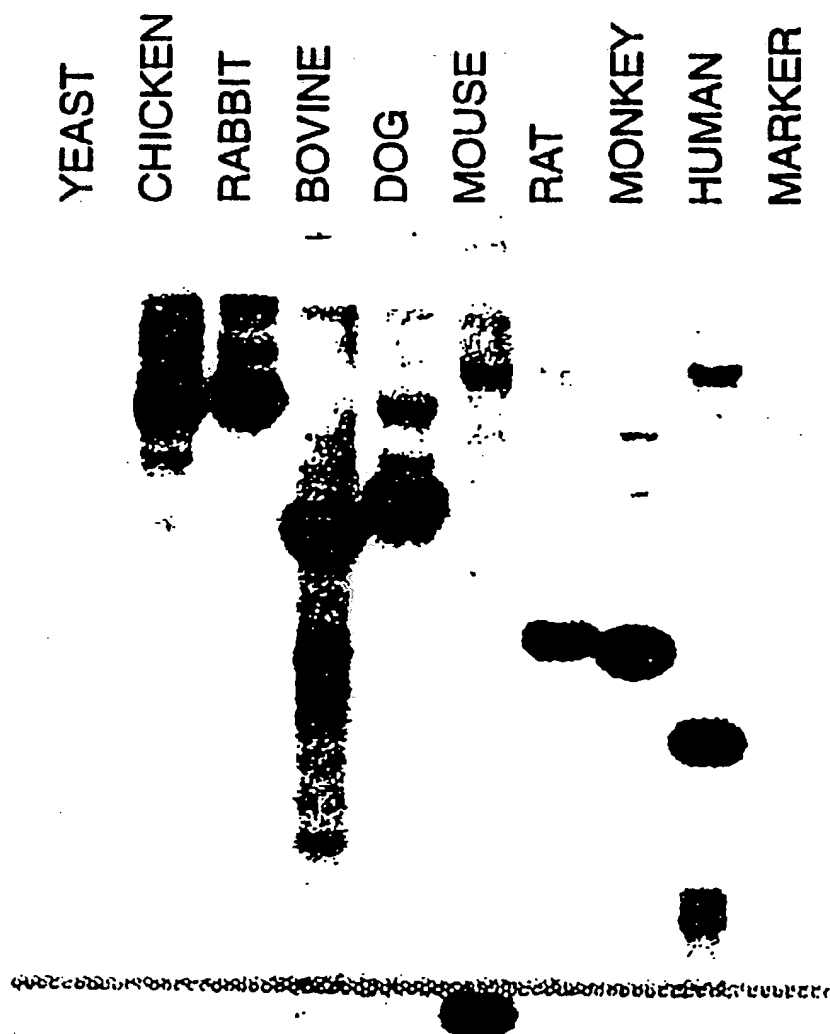
| | | | | | | | | | | | | | | | | | |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| CCTGCAG | CAT | CAA | GTG | TGG | GCG | GCG | AAA | GCC | GGG | GCG | TTG | AAG | AAG | GAC | TCG | CTG | 55 |
| | His | Gln | Val | Trp | Ala | Ala | Lys | Ala | Gly | Gly | Leu | Lys | Lys | Asp | Ser | Leu | |
| CTC | ACC | GTG | CGC | CTG | GGC | GCC | TGG | GGC | CAC | CCC | TTC | CCC | TCC | TGC | | 103 | |
| Leu | Thr | Val | Arg | Leu | Gly | Ala | Trp | Gly | His | Pro | Ala | Phe | Pro | Ser | Cys | | |
| GGG | CGC | CTC | AAG | GAG | GAC | AGC | AGG | TAC | ATC | TTC | ATG | GAG | CCC | GAG | | 151 | |
| Gly | Arg | Leu | Lys | Glu | Asp | Ser | Arg | Tyr | Ile | Phe | Met | Glu | Pro | Glu | | | |
| GCC | AAC | AGC | AGC | GGC | GGG | CCC | GGC | CGC | CTT | CCG | AGC | CTC | CTT | CCC | CCC | 199 | |
| Ala | Asn | Ser | Ser | Gly | Gly | Pro | Gly | Arg | Leu | Pro | Ser | Leu | Leu | Pro | Pro | | |
| TCT | CGA | GAC | GGG | CCG | GAA | CCT | CAA | GAA | GGT | CAG | CCG | GGT | GCT | GTG | | 247 | |
| Ser | Arg | Asp | Gly | Pro | Glu | Pro | Gln | Glu | Gly | Gln | Pro | Gly | Ala | Val | | | |
| CAA | CGG | TGC | GCC | TTG | CCT | CCC | CGC | TTG | AAA | GAG | ATG | AAG | AGT | CAG | GAG | 295 | |
| Gln | Arg | Cys | Ala | Leu | Pro | Pro | Arg | Leu | Lys | Glu | Met | Lys | Ser | Gln | Glu | | |
| TCT | GTG | GCA | GGT | TCC | AAA | CTA | GTG | CTT | CGG | TGC | GAG | ACC | AGT | TCT | GAA | 343 | |
| Ser | Val | Ala | Gly | Ser | Lys | Leu | Val | Leu | Arg | Cys | Glu | Thr | Ser | Ser | Glu | | |
| TAC | TCC | TCT | CTC | AAG | TTC | AAG | TGG | TTC | AAG | AAT | GGG | ACT | GAA | TTA | AGC | 391 | |
| Tyr | Ser | Ser | Leu | Lys | Phe | Lys | Trp | Phe | Lys | Asn | Gly | Ser | Glu | Leu | Ser | | |
| CGA | AAG | AAC | AAA | CCA | GAA | AAC | ATC | AAG | ATA | CAG | AAA | AGG | CCG | GGG | AAG | 439 | |
| Arg | Lys | Asn | Lys | Pro | Glu | Asn | Ile | Lys | Ile | Gln | Lys | Arg | Pro | Pro | Lys | | |
| TCA | GAA | CTT | CGC | ATT | AGC | AAA | CGC | TCA | CTG | GCT | GAT | TCT | GGA | GAA | TAT | 487 | |
| Ser | Glu | Leu | Arg | Ile | Ser | Lys | Ala | Ser | Leu | Ala | Asp | Ser | Gly | Glu | Tyr | | |

FIG. 28E

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP3

| | |
|--|------|
| ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC Met Cys Lys Val Ile Ser Lys Leu Gly <u>Asn Asp Ser</u> Ala Ser Ala <u>Asn</u> | 535 |
| ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA <u>Ile Arg</u> Ile Val Glu Ser <u>Asn Ala Thr</u> Ser Thr Ser Thr Ala Gly Thr | 583 |
| AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Cys Ala Glu Lys Thr Phe Cys Val Asn | 631 |
| GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser <u>Asn Pro Ser Arg Tyr</u> | 679 |
| TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr | 727 |
| GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Phe Leu Ser Leu Pro | 775 |
| GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCGATC TCCCCTCAGA TTCCGCGCTAG Glu | 838 |
| AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT GCCTGTGCGCA TGAGAACATT | 898 |
| AACACAAGCG ATTGTATGAC TTCTCTGTGC CGTGACTAGT GGGCTCTGAG CTACTCGTAG | 958 |
| GTGCGTAAGG CTCACAGTGT TCTGAAATTG ATCTTGAATT ACTGTGATAC GACATGATAG | 1018 |
| TCCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA GTCAAAAAAAA AAAAAAAA | 1078 |
| AAAAATCGAT GTCGACTCGA GATGTGGCTG | 1108 |

FIG. 29



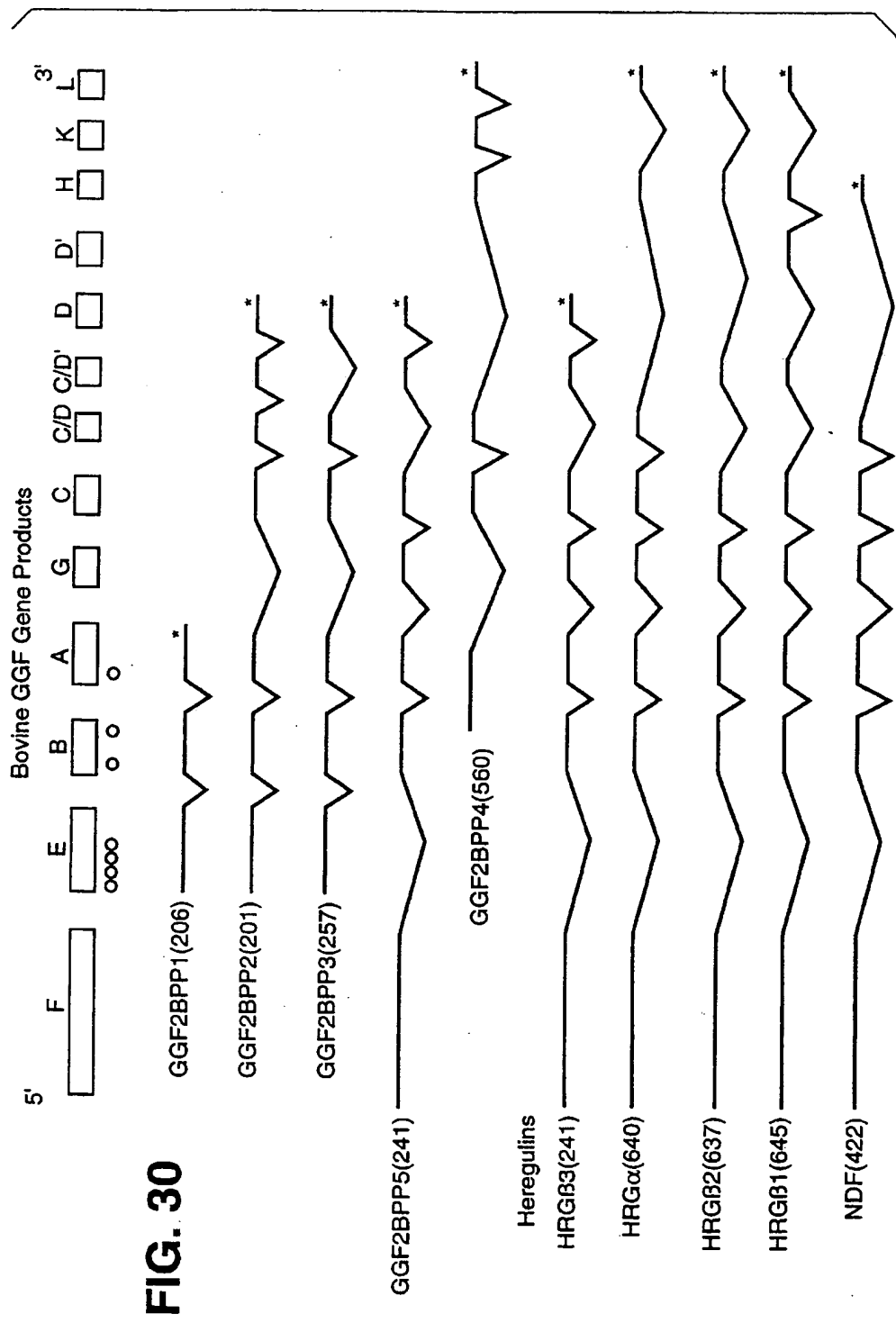


FIG. 30

FIG. 31A

Coding Segments of Glial Growth Factor/Heregulin Gene

CODING SEGMENT F: (SEQ ID NO: 136 (bovine) and 173 (human))

```

AGTTTCCCCC CCCTAACTGT CGGAACCTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC 60
GGCGGCTGCC CAGGCGGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCTCTGGGC 120
TGCAGAGCGG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC 180
CCAGCGGGGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC 240
AGTCCCAAGT GGCCCGGACC GCACGTTGCG TCCCGCGCGT CCGCGCGCGC GACAGGAGAC 300
GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTGCGTGG CCGGCTCTCA CTCCGGGGAC 360
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
CGCGAG CGCCTCAGCG CGGCGGCTCG CTCTC...CCC CTCGAGGGAC

AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTGCGCGG TCGCCTTCGC 420
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
AAACTTTTCC CAAACCCGAT CCGAGCCCTT GGACCAA...C TCGCCTTCGC

CGGAGCGCGT CCGCGCAGAG CGTGCACTTC TCGGCGGAG ATG TCG GAG CGC AGA 474
||| ||||||| ||||||| ||| ||| ||||||| ||| ||| ||| ||| |||
CGAGAGCGGT CCGCGTAGAG CGCTC.CGTC TCGGCGGAG ATG TCC GAG CGC AAA
K

Glu Gly Lys Gly Lys Gly Lys Gly Lys Lys Asp Arg Gly Ser Gly
GAA GGC AAA GGC AAG GGC AAG GGC AAG AAG GAC CGA GGC TCC GGC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
GAA GGC AGA GGC AAA GGC AAG GGC AAG AAG GAG CGA GGC TCC GGC
R K E

Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala
AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AAG AAG CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA G
E S

```

559

FIG. 31B

CODING SEGMENT E: (SEQ ID NO: 137)

| | |
|---|-----|
| CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG | 47 |
| His Gln Val Trp Ala Ala Lys Ala Gly Gly Lys Lys Asp Ser | |
| CTG CTC ACC GTG CGC CTG GGC GGC TGG GGC CAC CCC TTC CCC TCC | 95 |
| Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser | |
| TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC ATG GAG CCC | 143 |
| Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Met Glu Pro | |
| GAG GCC AAC AGC AGC GGC GGC CCC GGC CGC CTT CCG AGC CTC CTT CCC | 191 |
| Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Pro | |
| CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT | 239 |
| Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala | |
| GTG CAA CGG TGC G | 252 |
| Val Gln Arg Cys | |

FIG. 31D

CODING SEGMENT A: (SEQ ID NO: 139 (bovine) and 175 (human))

Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly
G AAG TCA GAA CTT CCG ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA
46
|||||

G AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA
N

Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT
94
|||||

GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT

Ala Asn Ile Thr Ile Val Glu Ser Asn Ala
GCC AAC ATC ACC ATT GTG GAG TCA AAC G
122
|||||

GCC AAT ATC ACC ATC GTG GAA TCA AAC G

FIG. 31E

CODING SEGMENT A': (SEQ ID NO: 140)

| | |
|---|-----|
| TCTAAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC | 60 |
| CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG | 110 |
| Lys Ser Glu Leu Arg Ile Ser Lys Ala | |
| TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA | 158 |
| Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu | |
| GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT | 206 |
| Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly | |
| AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC | 254 |
| Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile | |
| AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG | 302 |
| Lys Val Cys Gly His Thr | |
| TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT | 362 |
| GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATT | 417 |

FIG. 31F

CODING SEGMENT G: (SEQ ID NO: 141 (bovine) and 176 (human))

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Thr | Thr | Gly | Met | Pro | Ala | Ser | Thr | Glu | Thr | Ala | Tyr | Val | Ser |
| AG | ATC | ACC | ACT | GGC | ATG | CCA | GCC | TCA | ACT | GAG | ACA | GCG | TAT | GTG | TCT |
| | | | | | | | | | | | | | | | |
| AG | ATC | ATC | ACT | GGT | ATG | CCA | GCC | TCA | ACT | GAA | GGA | GCA | TAT | GTG | TCT |
| | | I | | | | | | | | | G | | | | |

| Ser | Glu | Ser | Pro | Ile | Arg | Ile | Ser | Val | Ser | Thr | Glu | Gly | Thr | Asn | Thr |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TCA | GAG | TCT | CCC | ATT | AGA | ATA | TCA | GTA | TCA | ACA | GAA | GGA | ACA | AAT | ACT |
| | | | | | | | | | | | | | | | |
| TCA | GAG | TCT | CCC | ATT | AGA | ATA | TCA | GTA | TCC | ACA | GAA | GGA | GCA | AAT | ACT |

| | | |
|-----|-----|-----|
| Ser | Ser | Ser |
| TCT | TCA | T |
| | | |
| TCT | TCA | T |

FIG. 31G

CODING SEGMENT C: (SEQ ID NO: 160 (bovine) and 177 (human))

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Thr | Ser | Thr | Ala | Gly | Thr | Ser | His | Leu | Val | Lys | Cys | Ala | |
| CC | ACA | TCC | ACA | TCT | ACA | GCT | GGG | ACA | AGC | CAT | CTT | GTC | AAG | TGT | GCA |
| | | | | | | | | | | | | | | | |
| CT | ACA | TCT | ACA | TCC | ACC | ACT | GGG | ACA | AGC | CAT | CTT | GTA | AAA | TGT | GCG |
| | | | | | | T | | | | | | | | | |
| Glu | Lys | Glu | Lys | Thr | Phe | Cys | Val | Asn | Gly | Gly | Glu | Cys | Phe | Met | Val |
| GAG | AAG | GAG | GAG | AAA | ACT | TTC | TGT | GTG | AAT | GGA | GGC | GAG | TGC | TTC | ATG |
| | | | | | | | | | | | | | | | |
| GAG | AAG | GAG | AAA | ACT | TTC | TGT | GTG | AAT | GGA | GGG | GAG | TGC | TTC | ATG | GTG |
| | | | | | | | | | | | | | | | |
| Lys | Asp | Leu | Ser | Asn | Pro | Ser | Arg | Tyr | Leu | Cys | | | | | |
| AAA | GAC | CTT | TCA | AAT | CCC | TCA | AGA | TAC | TTG | TGC | | | | | |
| | | | | | | | | | | | | | | | |
| AAA | GAC | CTT | TCA | AAC | CCC | TCG | AGA | TAC | TTG | TGC | | | | | |

47

95

128

FIG. 31H

CODING SEGMENT C/D: (SEQ ID NO: 142 (bovine) and 178 (human))

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Lys | Cys | Gln | Pro | Gly | Phe | Thr | Gly | Ala | Arg | Cys | Thr | Glu | Asn | Val | Pro | |
| AAG | TGC | CAA | CCT | GGA | TTC | ACT | GGA | GCG | AGA | TGT | ACT | GAG | AAT | GTG | CCC | 48 |
| | | | | | | | | | | | | | | | | |
| AAG | TGC | CAA | CCT | GGA | TTC | ACT | GGA | GCA | AGA | TGT | ACT | GAG | AAT | GTG | CCC | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|----|
| Met | Lys | Val | Gln | Thr | Gln | Glu | | | | | | | | | | |
| ATG | AAA | GTC | CAA | ACC | CAA | GAA | | | | | | | | | | 69 |
| | | | | | | | | | | | | | | | | |
| ATG | AAA | GTC | CAA | AAC | CAA | GAA | | | | | | | | | | |

N

FIG. 311

CODING SEGMENT D: (SEQ ID NO: 143 (bovine) and 179 (human))

| Lys | Cys | Pro | Asn | Glu | Phe | Thr | Gly | Asp | Arg | Cys | Gln | Asn | Tyr | Val | Met |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAG | TGC | CCA | AAT | GAG | TTT | ACT | GGT | GAT | CGC | TGC | CAA | AAC | TAC | GTA | ATG |
| | | | | | | | | | | | | | | | |
| AAG | TGC | CCA | AAT | GAG | TTT | ACT | GGT | GAT | CGC | TGC | CAA | AAC | TAC | GTA | ATG |

48

| | | | |
|-----|-----|-----|-----|
| Ala | Ser | Phe | Tyr |
| GCC | AGC | TTC | TAC |
| | | | |
| GCC | AGC | TTC | TAC |

60

FIG. 31J

CODING SEGMENT D: (SEQ ID NO: 144 (bovine) and 180 (human))

| Ser | Thr | Ser | Thr | Pro | Phe | Leu | Ser | Leu | Pro | Glu | * |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGT | ACG | TCC | ACT | CCC | TTT | CTG | TCT | CTG | CCT | GAA | TAG |
| | | | | | | | | | | | |
| AGT | ACG | TCC | ACT | CCC | TTT | CTG | TCT | CTG | CCT | GAA | TAG |

36

FIG. 31K

CODING SEGMENT D': (SEQ ID NO: 145 (bovine))

Lys His Leu Gly Ile Glu Phe Met Glu
AAG CAT CTT GGG ATT GAA TTT ATG GAG

27

CODING SEGMENT H: (SEQ ID NO: 146 (bovine) and 181 (human))

CODING SEGMENT H: (SEQ ID NO: 146 (bovine) and 181 (human))

Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr. Ile Thr Gly Ile
AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC. ATT ACC GGC ATT
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AAG GCG GAG GAG CTG CTG TAC CAG AAG AGA GTG CTG ACC. ATA ACC GGC ATC

| Cys | Ile | Ala | Leu | Leu | Val | Val | Gly | Ile | Met | Cys | Val | Val | Val | Tyr | Cys |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGC | ATC | GCG | CTG | CTC | GTG | GTT | GGC | ATC | ATG | TGT | GTG | GTG | GTC | TAC | TGC |
| | | | | | | | | | | | | | | | |
| TGC | ATC | GCC | CTC | CTT | GTG | GTC | GGC | ATC | ATG | TGT | GTG | GTG | GCC | TAC | TGC |

Lys Thr Lys Lys Lys Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AAAA ACC AAG AAA CAG CGG CGG AAA AAG CTG CAT GAC CGT CTT CGG CAG AGC

| Leu | Arg | Ser | Glu | Arg | Asn | Thr | Met | Met | Asn | Val | Ala | Asn | Gly | Pro | His |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTT | CGG | TCT | GAA | AGA | AAC | ACC | ATG | ATG | AAC | GTA | GCC | AAC | GGG | CCC | CAC |
| | | | | | | — | | | | — | | | | | |
| CTT | CGG | TCT | GAA | CGA | AAC | AAT | ATG | ATG | AAC | ATT | GCC | AAT | GGG | CCT | CAC |
| | | | | | | N | | | | I | | | | | |

| His | Pro | Asn | Pro | Pro | Glu | Asn | Val | Gln | Leu | Val | Asn | Gln | Tyr | Val |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CAC | CCC | AAT | CCG | CCC | GAG | AAC | GTG | CAG | CTG | GTG | AAT | CAA | TAC | GTA |
| | | | | | | | | | | | | | | |
| CAT | CCT | AAC | CCA | CCC | GAG | AAT | GTC | CAG | CTG | GTG | AAT | CAA | TAC | GTA |

| Ser | Lys | Asn | Val | Ile | Ser | Ser | Glu | His | Ile | Val | Glu | Arg | Glu | Ala | Glu |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TCT | AAA | AAT | GTC | ATC | TCT | AGC | GAG | CAT | ATT | GTT | GAG | AGA | GAG | GCG | GAG |
| | | | | | | | | | | | | | | | |
| TTCT | AAA | AAC | GTC | ATC | TCC | AGT | GAG | CAT | ATT | GTT | GAG | AGA | GAA | GCA | GAG |

FIG. 31M

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Phe | Ser | Thr | Ser | His | Tyr | Thr | Ser | Thr | Ala | His | His | Ser | Thr | 336 |
| AGC | TCT | TTT | TCC | ACC | AGT | CAC | TAC | ACT | TCG | ACA | GCT | CAT | CAT | TCC | ACT | |
| | | | | | | | | | | | | | | | | |
| ACA | TCC | TTT | TCC | ACC | AGT | CAC | TAT | ACT | TCC | ACA | GCC | CAT | CAC | TCC | ACT | |
| T | | | | | | | | | | | | | | | | |
| Thr | Val | Thr | Gln | Thr | Pro | Ser | His | Ser | Trp | Ser | Asn | Gly | His | Thr | Glu | 384 |
| ACT | GTC | ACT | CAG | ACT | CCC | AGT | CAC | AGC | TGG | AGC | AAT | GGA | CAC | ACT | GAA | |
| | | | | | | | | | | | | | | | | |
| ACT | GTC | ACC | CAG | ACT | CCT | AGC | CAC | AGC | TGG | AGC | AAC | GGA | CAC | ACT | GAA | |
| | | | | | | | | | | | | | | | | |
| Ser | Ile | Ile | Ser | Glu | Ser | His | Ser | Val | Ile | Val | Met | Ser | Ser | Val | Glu | 432 |
| AGC | ATC | ATT | TCG | GAA | AGC | CAC | TCT | GTC | ATC | GTG | ATG | TCA | TCC | GTA | GAA | |
| | | | | | | | | | | | | | | | | |
| AGC | ATC | CTT | TCC | GAA | AGC | CAC | TCT | GTA | ATC | GTG | ATG | TCA | TCC | GTA | GAA | |
| L | | | | | | | | | | | | | | | | |
| Asn | Ser | Arg | His | Ser | Pro | Thr | Gly | Gly | Pro | Arg | Gly | Arg | Leu | Asn | | 480 |
| AAC | AGT | AGG | CAC | AGC | AGC | CCG | ACT | GGG | GGC | CCG | AGA | GGA | CGT | CTC | AAT | |
| | | | | | | | | | | | | | | | | |
| AAC | AGT | AGG | CAC | AGC | AGC | CCA | ACT | GGG | GGC | CCA | AGA | GGA | CGT | CTT | AAT | |
| | | | | | | | | | | | | | | | | |
| Gly | Leu | Gly | Gly | Pro | Arg | Glu | Cys | Asn | Ser | Phe | Leu | Arg | His | Ala | Arg | 528 |
| GGC | TTG | GGA | GGC | CCT | CGT | GAA | TGT | AAC | AGC | TTC | CTC | AGG | CAT | GCC | AGA | |
| | | | | | | | | | | | | | | | | |
| GGC | ACA | GGA | GGC | CCT | CGT | GAA | TGT | AAC | AGC | TTC | CTC | AGG | CAT | GCC | AGA | |
| T | | | | | | | | | | | | | | | | |
| Glu | Thr | Pro | Asp | Ser | Tyr | Arg | Asp | Ser | Pro | His | Ser | Glu | Arg | | | 569 |
| GAA | ACC | CCT | GAC | TCC | TAC | CGA | GAC | TCT | CCT | CAT | AGT | GAA | AG | | | |
| | | | | | | | | | | | | | | | | |
| GAA | ACC | CCT | GAT | TCC | TAC | CGA | GAC | TCT | CCT | CAT | AGT | GAA | AG | | | |

FIG. 31N

CODING SEGMENT K: (SEQ ID NO: 161)

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| A | CAT | AAC | CTT | ATA | GCT | GAG | CTA | AGG | AGA | AAC | Asn | Lys | Ala | GCC | CAC | AGA | TCC | 46 |
| | His | Asn | Leu | Ile | Ala | Glu | Leu | Arg | Arg | Arg | Asn | Lys | Ala | His | His | Arg | Ser | |
| AAA | TGC | ATG | CAG | ATC | CAG | CTT | TCC | GCA | ACT | CAT | CTT | AGA | GCT | TCT | TCC | | 94 | |
| Lys | Cys | Met | Gln | Ile | Gln | Leu | Ser | Ala | Thr | His | Leu | Arg | Ala | Ser | Ser | | | |
| ATT | CCC | CAT | TGG | GCT | TCA | TTC | TCT | AAG | ACC | CCT | TGG | CCT | TTA | GGA | AG | | 141 | |
| Ile | Pro | His | Trp | Ala | Ser | Phe | Ser | Lys | Thr | Pro | Trp | Pro | Leu | Gly | Arg | | | |

46

94

| | Phe | His | Thr | Pro | Ser | Ser | Pro | Lys | Ser | Pro | Pro | Ser | Glu | Met | Ser | Pro |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TTC | CAC | ACG | CCA | AGC | TCC | CCC | CCC | AAG | TCA | CCC | CCT | TCG | GAA | ATG | TCC | CCG |
| | | | | | | | | | | | | | | | | |
| TTC | CAC | ACG | CCA | AGC | TCC | CCC | CCC | AAA | TCG | CCC | CCT | TCG | GAA | ATG | TCT | CCA |

142

| Pro | Val | Ser | Ser | Thr | Thr | Thr | Val | Ser | Met | Pro | Ser | Met | Ala | Val | Ser | Pro |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CCC | GTG | TCC | AGC | ACG | ACG | ACG | GTC | TCC | ATG | CCC | TCC | ATG | GCG | GTC | AGT | CCC |
| | | | | | | | | | | | | | | | | |
| CCC | GTG | TCC | AGC | ATG | ACG | ACG | GTG | TCC | ATG | CCT | TCC | ATG | GCG | GTC | AGC | CCC |

190

[illegible]

238

| Arg | Glu | Lys | - | Tyr | Asp | His | His | Ala | Gln | Phe | Asn | Ser | Phe | His |
|-----|-----|-----|------------------|------------------|-----|-----|-----|------------------|-----|-----|-----|-----|-----|-----|
| CGG | GAG | AAG | ... | TAT | GAC | CAC | CAC | GCC | CAG | CAA | TTC | AAC | TCG | TTC |
| | | | | | | | | | | | | | | |
| CGG | GAG | AAG | AAG _K | TTT _F | GAC | CAT | CAC | CCT _P | CAG | CAG | TTC | AGC | TCC | TTC |

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Asn | Pro | Ala | His | Glu | Ser | Asn | Ser | Leu | Pro | Pro | Ser | Pro | Leu | Arg |
| TGC | AAC | CCC | GCG | CAT | GAG | AGC | AAC | AGC | CTG | CCC | CCC | AGC | CCC | TTG | AGG |
| | | | | | | | | | | | | | | | |
| CAC | AAC | CCC | GCG | CAT | GAC | AGT | AAC | AGC | CTC | CCT | GCT | AGC | CCC | TTG | AGG |
| N | | | | D | | | | | | | A | | | | |

[illegible]

FIG. 31Q

| | |
|---|-----|
| Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala | 526 |
| GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC | |
| | |
| GTA GGT GAA GAT ACG CCT TTC CTG GGC ATA CAG AAC CCC CTG GCA GCC | |
| | |
| Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn | 574 |
| AGT CTC GAG GCG GCC CCT GCT GGC TTC CGC CTG GTC GAC AGC AGG ACT AAC | |
| | |
| AGT CTT GAG GCA ACA CCT GCT GGC TTC CGC CTG GCT GAC AGC AGG ACT AAC | |
| | |
| Pro Thr Gly Gly Phe Ser Pro Gln Glu Leu Gln Ala Arg Leu Ser | 622 |
| CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA GAA ATC CAG GCC AGG CTC TCC | |
| | |
| CCA GCA GGC CGC TTC TCG ACA CAG GAA GAA ATC CAG GCC AGG CTG TCT | |
| | |
| Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val * | 672 |
| GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAA AAC CGA AAT ACA | |
| | |
| AGT GTA ATT GCT AAC CAA GAC CCT ATT GCT GTA TAA AAC CTA AAT AAA | |
| | |
| CCC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA | 718 |
| | |
| CAC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA | |
| | |
| CCT TAA ATT AAA CAA | |
| | |
| CCT TAA ATT AAA CAA | |

FIG. 31R

HUMAN CODING SEGMENT E:
(SEQ ID NO: 163)

| | |
|---|-----|
| ATG AGA TGG CGA CGC GCG CCG CCG GCG TCC GGG CGT CCC GGC CCC CGG | 48 |
| Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg | |
| GCC CAG CGC CCC GGC TCC GCC GCG TCG TCG CCG CCG CTG CCG CTG | 96 |
| Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu | |
| CTG CCA CTA CTG CTG CTG GCG ACC ACC GCG GCC CTG GCG CCG GGG GCG | 144 |
| Leu Pro Leu Leu Leu Leu Leu Leu Thr Ala Ala Leu Ala Pro Gly Ala | |
| GCG GCC GGC AAC GAG GCG GGT CCC GCG GGG GCC TCG GTG TGC TAC TCG | 192 |
| Ala Ala Gly Asn Glu Ala Ala Pro Ala Pro Ala Ser Val Cys Tyr Ser | |
| TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG GCG GCC GCG | 240 |
| Ser Pro Pro Ser Val Gly Ser Val Gln Gln Leu Ala Gln Arg Ala Ala | |
| GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CCG CAG CAG GGG GCA | 288 |
| Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala | |
| CTC GAC AGG AAG GCG GCG GCG GCG GCG GAG GCA GGG GCG TGG GCG | 336 |
| Leu Asp Arg Lys Ala Ala Ala Ala GCG CCA CCG GCG CTG GGG CCG CCC | 384 |
| GGC GAT CGC GAG CCG CCA GCC GCG GCG CCA CCG GCG CTG GGG CCG CCC | |
| Gly Asp Arg Glu Pro Pro Ala Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro | |
| GCC GAG GAG CCG CTG CTC GCC GCG AAC GCG ACC GTG CCC TCT TGG CCC | 432 |
| Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro | |
| ACC GCC CCG GTG CCC AGC GCC GCG GAG CCC GGG GAG GCG CCC TAT | 480 |
| Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Ala Pro Tyr | |
| CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GCG TTG AAG | 528 |
| Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Leu Lys | |
| AAG GAC TCG CTG CTC ACC GTG CCG CTG GGG ACC TGG GCG CAC CCC GCC | 576 |
| Lys Asp Ser Leu Leu Thr Val Arg Leu Leu Gly Thr Trp Gly His Pro Ala | |
| TTC CCC TCC TGC GGG AGG CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC | 624 |
| Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe | |
| ATG GAG CCC GAC GCC AAC AGC ACC AGC CCG GCG CCG GCC TTC CGA | 672 |
| Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Phe Arg | |
| GCC TCT TTC CCT CTG GAG ACG GCG CCG AAC CTC AAG AAG GAG GTC | 720 |
| Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Glu Val | |
| AGC CGG GTG CTG TGC AAG CCG TGC G | 745 |
| Ser Arg Val Leu Cys Lys Arg Cys | |

FIG. 32A

GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence

SEQ ID NO: 148:

| | | | | | | |
|-------------|-----------------------------|---------------------------------|-------------|---------------------|------------|-----|
| AGTTTCCCCC | CCCAACTTGT | CGGAACCTCTG | GGCTCGCGCG | CAGGGCAGGA | GCGGAGCGGC | 60 |
| GGCGGCTGCC | CAGGCGATGC | GAGCGCGGGC | CGGACGGTAA | TGCGCTCTCC | CTCCTCGGGC | 120 |
| TGCGAGCGCG | CCGGACCGAG | GCAGCGACAG | GAGCGGACCG | CGGCGGGAAC | CGAGGACTCC | 180 |
| CCAGCGGCGC | GCCAGCAGGA | GCCACCCCGC | GAGCGTGCGA | CCGGGACGGA | GCGCCCCCCA | 240 |
| GTCCACAGGTG | GCCCCGACCG | CACGTTGCGT | CCCCCGCGCTC | CCCCCGGGCG | ACAGGAGACG | 300 |
| CTCCCCCCCCA | CGCGCGCGCG | GCCTCGGCC | GGTCGCTGGC | CCGCCCTCCAC | TCCGGGGACA | 360 |
| AACTTTTCCC | GAAGCCGATC | CCAGCCCTCG | GACCCAAACT | TGTCGCGCGT | CGCCTTCGCC | 420 |
| GGGAGCCGTC | CGCGCAGAGC | GTGCACTTCT | CGGGCGAG | ATG TCG GAG CGC AGA | | 475 |
| | | | | Met Ser Glu Arg Arg | | |
| GAA GGC AAA | GGC AAG GGG AAG GGC GGC | AAG AAG AAG GAC CGA GGC TCC GGG | | | | 523 |
| Glu Gly Lys | Gly Lys Gly Lys Gly Lys | Lys Lys Asp Arg Gly Ser Gly | | | | |
| AAG AAG CCC | GTG CCC GCG GCT GGC GGC | CCG AGC CCA GCC TTG CCT CCC | | | | 571 |
| Lys Lys Pro | Val Pro Ala Ala Gly Gly | Pro Ser Pro Ala Leu Pro Pro | | | | |
| CGC TTG AAA | GAG ATG AAG ATG CAG GAG | TCT GTG GCA GGT TCC AAA CTA | | | | 619 |
| Arg Leu Lys | Glu Met Lys Ser Gln Glu Ser | Val Ala Gly Ser Lys Leu | | | | |
| GTG CTT CGG | TGC GAG ACC AGT TCT GAA TAC | TCT CTC AAG TTC AAG | | | | 667 |
| Val Leu Arg | Cys Glu Thr Ser Ser Ser | Glu Tyr Ser Ser Leu Lys Phe Lys | | | | |
| TGG TTC AAG | AAT CGG AGT GAA TTA AGC CGA | AAG AAC AAA CCA CAA AAC | | | | 715 |
| Trp Phe Lys | Asn Gly Ser Glu Leu Ser Arg | Lys Asn Lys Pro Gln Asn | | | | |
| ATC AAG ATA | CAG AAA AGG CCG GGG AAG TCA | GAA CTT CGC ATT AGC AAA | | | | 763 |
| Ile Lys Ile | Gln Lys Arg Pro Gly Lys | Ser Glu Leu Arg Ile Ser Lys | | | | |
| GCG TCA CTG | GCT GAT TCT GGA GAA TAT | ATG TGC AAA GTG ATC AGC AAA | | | | 811 |
| Ala Ser Leu | Ala Asp Ser Gly Glu Tyr Met | Cys Lys Val Ile Ser Lys | | | | |

FIG. 32B

GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence

| | |
|--|------|
| CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn | 859 |
| GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser | 907 |
| TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr | 955 |
| TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG Ser Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys | 1003 |
| TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe | 1051 |
| ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA Met Val Lys Asp Leu Ser Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Cys Pro | 1099 |
| AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe | 1147 |
| TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu | 1193 |
| CTCAGTCGGT GCGGCTTTCT TGTGCGGCA TCTCCCTCA GATTCAACCT AGAGCTAGAT | 1253 |
| GCGTTTACC AGGTCTAACA TTGACTGCCT CTGCTGTGTCG CATGAGAACA TTAACACAAG | 1313 |
| CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA | 1373 |
| GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTTACTGTGAT ACGACATGAT AGTCCCTCTC | 1433 |
| ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAAT | 1493 |
| CGTTCCACGG GACAGTCCCT CTTCCTTATA AAATGACCCCT ATCCTTGAAA AGGAGGTGTG | 1553 |
| TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT | 1613 |
| TCTTTCTGAC AAATAAACAG AATAAAAAAA AAAAAAAAAA A | 1654 |

FIG. 33A

GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence

SEQ ID NO: 149:

| | |
|---|-----|
| CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG | 48 |
| His Gln Val Trp Ala Ala Lys Ala Gly Leu Lys Lys Asp Ser Leu | |
| CTC ACC GTG CGC CTG GGC GGC TGG GGC CAC CCC GGC TTC CCC TCC TGC | 96 |
| Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys | |
| GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG | 144 |
| Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu | |
| GCC AAC AGC AGC GGC GGC CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC | 192 |
| Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro | |
| TCT CGA GAC GGC CCG GAA CCT CAA GAA GGT CAG CCG GGT GCT GTG | 240 |
| Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gln Pro Gly Ala Val | |
| CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG | 288 |
| Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu | |
| TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA | 336 |
| Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu | |
| TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC | 384 |
| Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser | |
| CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG | 432 |
| Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys | |
| TCA GAA CTT CGC ATT AGC AAA CCG TCA CTG GCT GAT TCT GGA GAA TAT | 480 |
| Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr | |
| ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC | 528 |
| Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn | |

FIG. 33B

GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence

| | |
|--|------|
| ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr | 576 |
| AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn | 624 |
| GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr | 672 |
| TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT Leu Cys Lys Cys Gln Pro Gly Phe Thr Thr Gly Ala Arg Cys Thr Glu Asn | 720 |
| GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT Val Pro Met Lys Val Gln Thr Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr | 768 |
| GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser | 816 |
| ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTCTTG Thr Pro Phe Leu Ser Leu Pro Glu | 870 |
| TTGCCGCATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT | 930 |
| GACTGCCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC | 990 |
| CGTGACTAGT GGGCTCTGAG CTA CTCTCGTAG GTGCGTAAGG CTCCAGTCTT TCTGAAATTG | 1050 |
| ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG | 1110 |
| GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA | 1140 |

FIG. 34A

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

SEQ ID NO: 150:

| | |
|---|-----|
| G AAG TCA GAA CTT CGC ATT AGC AAA CCG TCA CTG GCT GAT TCT GGA GAA | 49 |
| Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu | |
| TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC | 97 |
| Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala | |
| AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG | 145 |
| Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly | |
| ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG | 193 |
| Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val | |
| AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA | 241 |
| Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg | |
| TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG | 289 |
| Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu | |
| AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC | 337 |
| Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Leu Tyr | |
| CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG | 385 |
| Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val | |
| GTT GGC ATC ATG TGT GTG GTC TAC TGC AAA ACC AAG AAA CAA CCG | 433 |
| Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg | |
| AAA AAG CTT CAT GAC CCG CTT CCG CAG AGC CTT CCG TCT GAA AGA AAC | 481 |
| Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn | |
| ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC | 529 |
| Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro | |
| GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT | 577 |
| Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser | |

FIG. 34B

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

| | |
|--|------|
| AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser | 625 |
| CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT ACT GTC ACT CAG ACT CCC His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro | 673 |
| AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC Ser His Ser Ser Trp Ser Ser Asn Gly His Thr Glu Ser Ile Ile Ser Glu Ser | 721 |
| CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser | 769 |
| CCG ACT GGC GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg | 817 |
| GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC Glu Cys Asn Ser Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr | 865 |
| CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg | 913 |
| AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala | 961 |
| ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys | 1009 |
| ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT Thr Pro Trp Pro Leu Gly Arg Tyr Val Ser Ala Met Thr Thr Pro Ala | 1057 |
| CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro | 1105 |
| CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG AGC GTC TCC ATG CCC Pro Ser Glu Met Ser Pro Pro Val Ser Ser Thr Thr Val Ser Met Pro | 1153 |

FIG. 34C

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

| | |
|---|------|
| TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT | 1201 |
| Ser Met Ala Val Ser Pro Phe Val Glu Glu Arg Pro Leu Leu Leu | |
| GTG ACG CCA CCA CGG CTG CCG GAG AAG TAT GAC CAC CAC GCC CAG CAA | 1249 |
| Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His His Ala Gln Gln | |
| TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC | 1297 |
| Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro | |
| CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG | 1345 |
| Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Tyr Glu Thr Thr Gln | |
| GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC | 1393 |
| Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser | |
| CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG | 1441 |
| Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu | |
| GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA | 1489 |
| Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu | |
| ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG | 1537 |
| Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln | |
| AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GGC TTC CGC CTG GTC | 1585 |
| Asn Pro Leu Ala Ala Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val | |
| GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG | 1633 |
| Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu | |
| CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC | 1681 |
| Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val | |
| TAAACCGAA ATACACCCAT AGATTACCT GTAAACCTTT ATTTTATATA ATAAAGTATT | 1741 |
| CCACCTTAAA TTAAACAAA AAA | 1764 |

FIG. 35

| | | | | | | |
|----------|------------------|---|---|---|---|---|
| GGF2bpp5 | (SEQ ID NO: 151) | KCAEKEKTFVCVNGGECFMVKDLSPSPRYLCKCPNEFTGDRQCQYVMAFY | * | * | * | * |
| GGF2bpp4 | (SEQ ID NO: 152) | KCAEKEKTFVCVNGGDCFMVKDLSPSPRYLCKCQPGFTGARTENVPMKVQ | | | | |
| hEGF | (SEQ ID NO: 153) | ECLRKYKDFCIH-GECKYVKELRAPSP---CKCQOEYFGERCGEKSNKTHS | | | | |

FIG. 36
200 kDa Tyrosine Phosphorylation
Compared with Mitogenic Activity

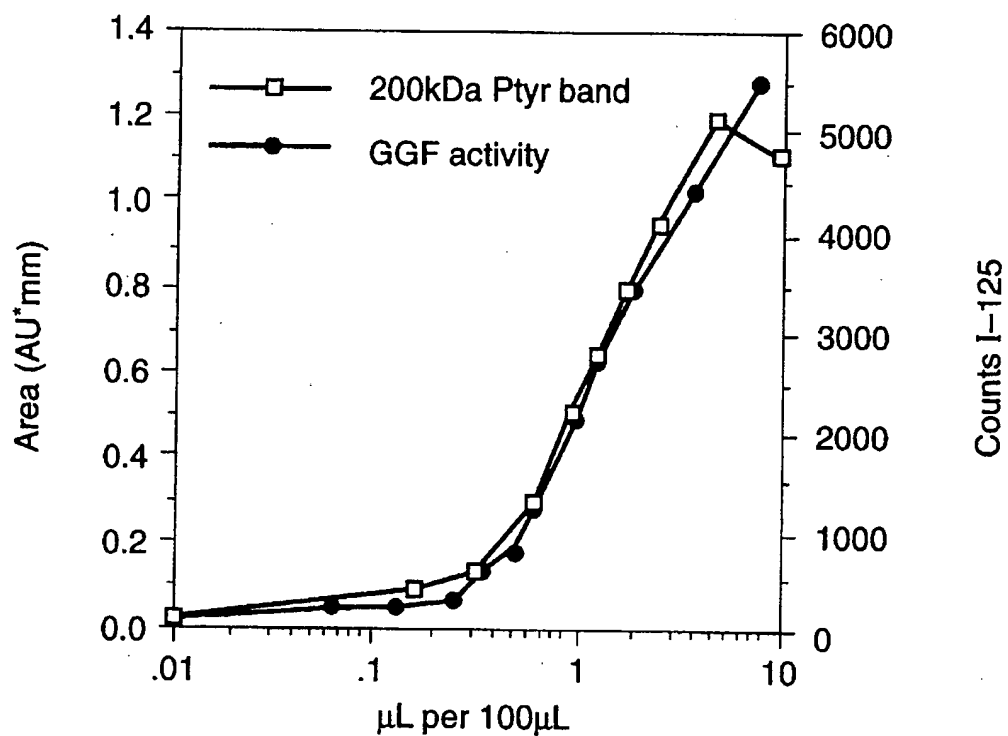


FIG. 37A GGF/Heregulin Splicing Variants

F-B-A'

F-B-A-C-C/D-D
F-B-A-C-C/D-H
F-B-A-C-C/D-H-L
F-B-A-C-C/D-H-K-L
F-B-A-C-C/D-D'-H
F-B-A-C-C/D-D'-H-L
F-B-A-C-C/D-D'-H-K-L
F-B-A-C-C/D'-D
F-B-A-C-C/D'-H
F-B-A-C-C/D'-H-L
F-B-A-C-C/D'-H-K-L
F-B-A-C-C/D'-D'-H
F-B-A-C-C/D'-D'-H-L
F-B-A-C-C/D'-D'-H-K-L
F-B-A-C-C/D-C/D'-D
F-B-A-C-C/D-C/D'-H
F-B-A-C-C/D-C/D'-H-L
F-B-A-C-C/D-C/D'-H-K-L
F-B-A-C-C/D-C/D'-D'-H
F-B-A-C-C/D-C/D'-D'-H-L
F-B-A-C-C/D-C/D'-D'-H-K-L

F-B-A-G-C-C/D-D
F-B-A-G-C-C/D-H
F-B-A-G-C-C/D-H-L
F-B-A-G-C-C/D-H-K-L
F-B-A-G-C-C/D-D'-H
F-B-A-G-C-C/D-D'-H-L
F-B-A-G-C-C/D-D'-H-K-L
F-B-A-G-C-C/D'-D
F-B-A-G-C-C/D'-H
F-B-A-G-C-C/D'-H-L
F-B-A-G-C-C/D'-H-K-L
F-B-A-G-C-C/D'-D'-H
F-B-A-G-C-C/D'-D'-H-L
F-B-A-G-C-C/D'-D'-H-K-L
F-B-A-G-C-C/D-C/D'-D
F-B-A-G-C-C/D-C/D'-H
F-B-A-G-C-C/D-C/D'-H-L
F-B-A-G-C-C/D-C/D'-H-K-L
F-B-A-G-C-C/D-C/D'-D'-H
F-B-A-G-C-C/D-C/D'-D'-H-L
F-B-A-G-C-C/D-C/D'-D'-H-K-L

F-E-B-A'

F-E-B-A-C-C/D-D
F-E-B-A-C-C/D-H
F-E-B-A-C-C/D-H-L
F-E-B-A-C-C/D-H-K-L
F-E-B-A-C-C/D-D'-H
F-E-B-A-C-C/D-D'-H-L
F-E-B-A-C-C/D-D'-H-K-L
F-E-B-A-C-C/D'-D
F-E-B-A-C-C/D'-H
F-E-B-A-C-C/D'-H-L
F-E-B-A-C-C/D'-H-K-L
F-E-B-A-C-C/D'-D'-H
F-E-B-A-C-C/D'-D'-H-L
F-E-B-A-C-C/D'-D'-H-K-L
F-E-B-A-C-C/D-C/D'-D
F-E-B-A-C-C/D-C/D'-H
F-E-B-A-C-C/D-C/D'-H-L
F-E-B-A-C-C/D-C/D'-H-K-L
F-E-B-A-C-C/D-C/D'-D'-H
F-E-B-A-C-C/D-C/D'-D'-H-L
F-E-B-A-C-C/D-C/D'-D'-H-K-L

F-E-B-A-G-C-C/D-D
F-E-B-A-G-C-C/D-H
F-E-B-A-G-C-C/D-H-L
F-E-B-A-G-C-C/D-H-K-L
F-E-B-A-G-C-C/D-D'-H
F-E-B-A-G-C-C/D-D'-H-L
F-E-B-A-G-C-C/D-D'-H-K-L
F-E-B-A-G-C-C/D'-D
F-E-B-A-G-C-C/D'-H
F-E-B-A-G-C-C/D'-H-L
F-E-B-A-G-C-C/D'-H-K-L
F-E-B-A-G-C-C/D'-D'-H
F-E-B-A-G-C-C/D'-D'-H-L
F-E-B-A-G-C-C/D'-D'-H-K-L
F-E-B-A-G-C-C/D-C/D'-D
F-E-B-A-G-C-C/D-C/D'-H
F-E-B-A-G-C-C/D-C/D'-H-L
F-E-B-A-G-C-C/D-C/D'-H-K-L
F-E-B-A-G-C-C/D-C/D'-D'-H
F-E-B-A-G-C-C/D-C/D'-D'-H-L
F-E-B-A-G-C-C/D-C/D'-D'-H-K-L

FIG. 37B
GGF/Heregulin
Splicing Variants

E-B-A'

E-B-A-C-C/D-D
E-B-A-C-C/D-H
E-B-A-C-C/D-H-L
E-B-A-C-C/D-H-K-L
E-B-A-C-C/D-D'-H
E-B-A-C-C/D-D'-H-L
E-B-A-C-C/D-D'-H-K-L
E-B-A-C-C/D'-D
E-B-A-C-C/D'-H
E-B-A-C-C/D'-H-L
E-B-A-C-C/D'-H-K-L
E-B-A-C-C/D'-D'-H
E-B-A-C-C/D'-D'-H-L
E-B-A-C-C/D'-D'-H-K-L
E-B-A-C-C/D-C/D'-D
E-B-A-C-C/D-C/D'-H
E-B-A-C-C/D-C/D'-H-L
E-B-A-C-C/D-C/D'-H-K-L
E-B-A-C-C/D-C/D'-D'-H
E-B-A-C-C/D-C/D'-D'-H-L
E-B-A-C-C/D-C/D'-D'-H-K-L

E-B-A-G-C-C/D-D
E-B-A-G-C-C/D-H
E-B-A-G-C-C/D-H-L
E-B-A-G-C-C/D-H-K-L
E-B-A-G-C-C/D-D'-H
E-B-A-G-C-C/D-D'-H-L
E-B-A-G-C-C/D-D'-H-K-L
E-B-A-G-C-C/D'-D
E-B-A-G-C-C/D'-H
E-B-A-G-C-C/D'-H-L
E-B-A-G-C-C/D'-H-K-L
E-B-A-G-C-C/D'-D'-H
E-B-A-G-C-C/D'-D'-H-L
E-B-A-G-C-C/D'-D'-H-K-L
E-B-A-G-C-C/D-C/D'-D
E-B-A-G-C-C/D-C/D'-H
E-B-A-G-C-C/D-C/D'-H-L
E-B-A-G-C-C/D-C/D'-H-K-L
E-B-A-G-C-C/D-C/D'-D'-H
E-B-A-G-C-C/D-C/D'-D'-H-L
E-B-A-G-C-C/D-C/D'-D'-H-K-L

FIG. 38

EGFL1

SEQ. ID NO: 154:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGC | CAT | CTT | GTC | AAG | TGT | GCA | GAG | AAG | GAG | AAA | ACT | TTC | TGT | GTG | AAT | 48 |
| Ser | His | Leu | Val | Lys | Cys | Ala | Glu | Lys | Glu | Lys | Thr | Phe | Cys | Val | Asn | |
| GGA | GGC | GAG | TGC | TTC | ATG | GTG | AAA | GAC | CTT | TCA | AAT | CCC | TCA | AGA | TAC | 96 |
| Gly | Gly | Glu | Cys | Phe | Met | Val | Lys | Asp | Leu | Ser | Asn | Pro | Ser | Arg | Tyr | |
| TTG | TGC | AAG | TGC | CCA | AAT | GAG | TTT | ACT | GGT | GAT | CGC | TGC | CAA | AAC | TAC | 144 |
| Leu | Cys | Lys | Cys | Pro | Asn | Glu | Phe | Thr | Gly | Asp | Arg | Cys | Gln | Asn | Tyr | |
| GTA | ATG | GCC | AGC | TTC | TAC | AGT | ACG | TCC | ACT | CCC | TTT | CTG | TCT | CTG | CCT | 192 |
| Val | Met | Ala | Ser | Phe | Tyr | Ser | Thr | Ser | Thr | Pro | Phe | Leu | Ser | Leu | Pro | |

GAA TAG

Glu

198

FIG. 39 **EGFL2**

SEQ ID NO: 155:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGC | CAT | CTT | GTC | AAG | TGT | GCA | GAG | AAG | GAG | AAA | ACT | TTC | TGT | GTG | AAT | 48 |
| Ser | His | Leu | Val | Lys | Cys | Ala | Glu | Lys | Glu | Lys | Thr | Phe | Cys | Val | Asn | |
| GGA | GGC | GAG | TGC | TTC | ATG | GTG | AAA | GAC | CTT | TCA | AAT | CCC | TCA | AGA | TAC | 96 |
| Gly | Gly | Glu | Cys | Phe | Met | Val | Lys | Asp | Leu | Ser | Asn | Pro | Ser | Arg | Tyr | |
| TTG | TGC | AAG | TGC | CAA | CCT | GGA | TTC | ACT | GGA | GCG | AGA | TGT | ACT | GAG | AAT | 144 |
| Leu | Cys | Lys | Cys | Gln | Pro | Gly | Phe | Thr | Gly | Ala | Arg | Cys | Thr | Glu | Asn | |
| GTG | CCC | ATG | AAA | GTC | CAA | ACC | CAA | GAA | AAA | GCG | GAG | GAG | CTC | TAC | TAA | 192 |
| Val | Pro | Met | Lys | Val | Gln | Thr | Gln | Glu | Lys | Ala | Glu | Glu | Leu | Tyr | | |

FIG. 40

EGFL3

SEQ ID NO: 156:

| | |
|---|-----|
| AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT | 48 |
| Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn | |
| GGA GGC GAG TGC TTC ATG ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC | 96 |
| Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr | |
| TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC | 144 |
| Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr | |
| GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA | 183 |
| Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr | |

FIG. 41

EGFL4

SEQ ID NO: 157:

| | |
|---|-----|
| AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT | 48 |
| Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn | |
| GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC | 96 |
| Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr | |
| TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC | 144 |
| Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr | |
| GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA | 192 |
| Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys | |
| GCG GAG GAG CTC TAC TAA | 210 |
| Ala Glu Glu Leu Tyr | |

FIG. 42

EGFL5

SEQ ID NO: 158:

| | |
|---|-----|
| AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT | 48 |
| Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn | |
| GGA GGC GAG TGC TTC ATG ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC | 96 |
| Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr | |
| TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT | 144 |
| Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn | |
| GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT | 192 |
| Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr | |
| GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC AGC TTC TAC AGT ACG TCC | 240 |
| Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser | |
| ACT CCC TTT CTG TCT CTG CCT GAA TAG | 267 |
| Thr Pro Phe Leu Ser Leu Pro Glu | |

FIG. 43

EGFL6

SEQ ID NO: 159:

| | |
|---|-----|
| AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT | 48 |
| Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn | |
| GGA GGC GAG TGC TTC ATG ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC | 96 |
| Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr | |
| TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT | 144 |
| Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn | |
| GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT | 192 |
| Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr | |
| GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG | 240 |
| Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu | |
| GAG CTC TAC TAA | 252 |
| Glu Leu Tyr | |

FIG. 44
GGF2HBS5

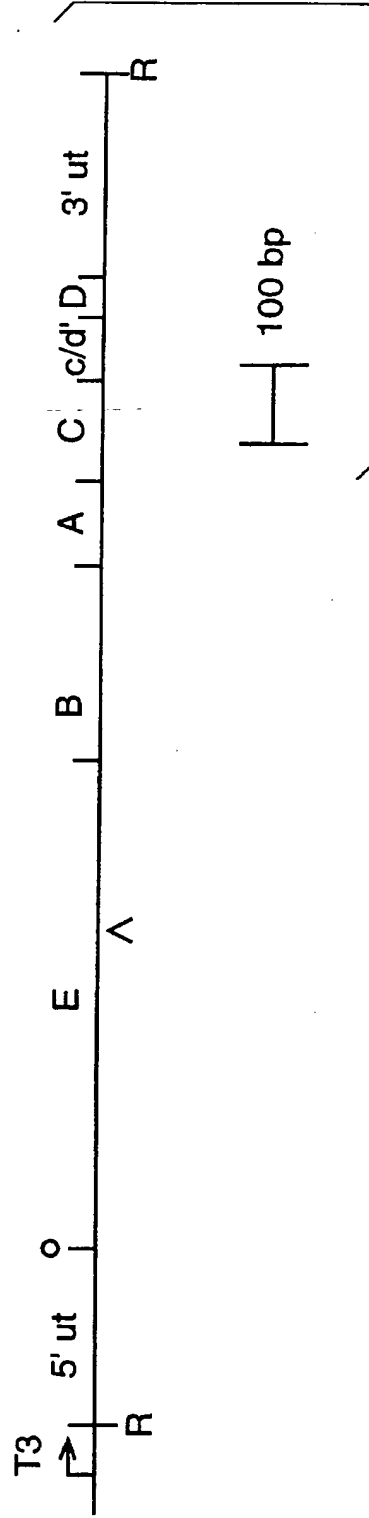


FIG. 45A

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

SEQ ID NO: 21:

| | | | | | | |
|-------------|-------------|--------------|-------------|-------------|-------------|---------|
| GGAATTCCTT | TTTTTTTTTT | TTTTTTTCTT | NNTTTTTTTT | TGCCCTTATA | CCTCTTCGCC | 60 |
| TTTCTGTGGT | TCCATCCACT | TCTTCCCCCT | CCTCCTCCCA | TAAACAACATC | TCCTACCCCT | 120 |
| GCACCCCCAA | TAAATAAATA | AAAGGAGGAG | GGCAAGGGGG | GAGGAGGAGG | AGTGGTGCTG | 180 |
| CGAGGGGAAG | GAAAAGGGAG | GCAGCGCGAG | AAGAGCCGGG | CAGAGTCCGA | ACCGACAGCC | 240 |
| AGAAGCCCCG | ACGCACCTCG | CACC ATG AGA | TGG CGA | CGC GCC | CCG CGC CGC | 291 |
| | | Met Arg Trp | Arg Arg Ala | Pro Arg Arg | | |
| TCC GGG CGT | CCC GGC CCC | CGG GCC | CAG CGC | CCC GGC | TCC GCC | GCC CGC |
| Ser Gly Arg | Pro Gly Pro | Arg Ala Gln | Arg Pro | Gly Ser | Ala Ala | Arg |
| TCG TCG CCG | CTG CCG | CTG CTA | CTG CTA | CTG CTG | CTG GGG | ACC |
| Ser Ser Pro | Pro Leu Pro | Leu Leu | Leu Leu | Leu Leu | Gly Thr | |
| | | Val Cys | Leu Leu | Thr Val | | |
| | | | | | GGF-II | 09 |
| GCG GCC CTG | GCG CCG | GCG GCC | GCG AAC | GAG GCG | GCT CCC | GCG |
| Ala Ala Leu | Ala Pro | Gly Ala | Ala Gly | Asn Glu | Ala Pro | Ala |
| Ala Ala Leu | Pro Pro | | | | | |
| GGG GCC TCG | GTG TGC | TAC TCG | TCC CCG | CCC AGC | GTG GGA | TCG GTG |
| Gly Ala Ser | Val Cys | Tyr Ser | Pro Pro | Pro Ser | Val Gly | Ser Val |
| | | Ala Ser | Pro Val | Ser Val | Gly Ser | Val Gln |
| | | | | | | GGF-II |
| | | | | | | 08 |
| GAG CTA GCT | CAG CGC | GCC GCG | GTG GTG | ATC GAG | GGA AAG | GTG CAC |
| Glu Leu Ala | Gln Arg | Ala Ala | Val Val | Ile Glu | Gly Lys | Val His |
| Glu Leu Val | Gln Arg | Trp Phe | Val Val | Ile Glu | Gly Lys | Lys |
| | | | | | | GGF-II |
| | | | | | | 04 |
| | | | | | | 531 |

FIG. 45B

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

| | |
|---|-----|
| CAG CGG CGG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG | 579 |
| Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala | |
| GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GGC | 627 |
| Gly Glu Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly | |
| CCA CGG GCG CTG GGG CCG CCC GCG GAG GAG CCG CTG CTC GCC AAC | 675 |
| Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Ala Ala Asn | |
| GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GCG GAG | 723 |
| Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu | |
| CCC GGG GAG GAG GCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG | 771 |
| Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala | |
| Lys Val His Glu Val Trp Ala GGF-II 01 & GGF-II 11 | |
| GTG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG CTC ACC GTG CGC CTG | 819 |
| Val Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu | |
| Ala Lys Asp Leu Leu Leu Xaa Val GGF-II 10 | |
| GGG ACC TGG GGC CAC CCC GCC TTC CCC TCC TGC GGG AGG CTC AAG GAG | 867 |
| Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu | |
| Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr GGF-II 03 | |
| GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC | 915 |
| Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser | |
| Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly GGF-II 02 | |

FIG. 45C

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

| | |
|--|------|
| CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly | 963 |
| CGG AAC CTC AAG AAG GAG GTC AGC CGG GTG CTG TGC AAG CGG TGC GCC Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala | 1011 |
| TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly | 1059 |
| TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Leu Val Leu Arg GGF-II 06 | 1107 |
| AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA Arg Phe Lys Lys Trp Phe Lys Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys | 1155 |
| CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg | 1203 |
| ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys GGF-II 12 | 1251 |
| ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG Ile Ser Lys Lys Leu Gly Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val | 1299 |
| GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val | 1347 |

FIG. 45D

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

| | |
|--|------|
| AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC Lys Cys Ala Glu Lys Lys Thr Phe Cys Val Asn Gly Gly Glu Cys | 1395 |
| TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys | 1443 |
| CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser | 1491 |
| TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu | 1530 |
| TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTGCTGCA TCTCCCTCA GATTCCACCT | 1590 |
| AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCCTGTCG CATGAGAACA | 1650 |
| TTAACAAAAAG CAATTGTATT ACTTCCCTCTG TTCGGGACTA GTTGGCTCTG AGATACTAAT | 1710 |
| AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAAATTGAT | 1770 |
| AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA | 1830 |
| TAAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA | 1890 |
| AAGGGTGTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT | 1950 |
| CAGATGTGT TATTGTGCAC AAATAAACAT AATAAAAGGA AAAAAA AAA | 2003 |

FIG. 46
Schwann Cell Proliferation Assay

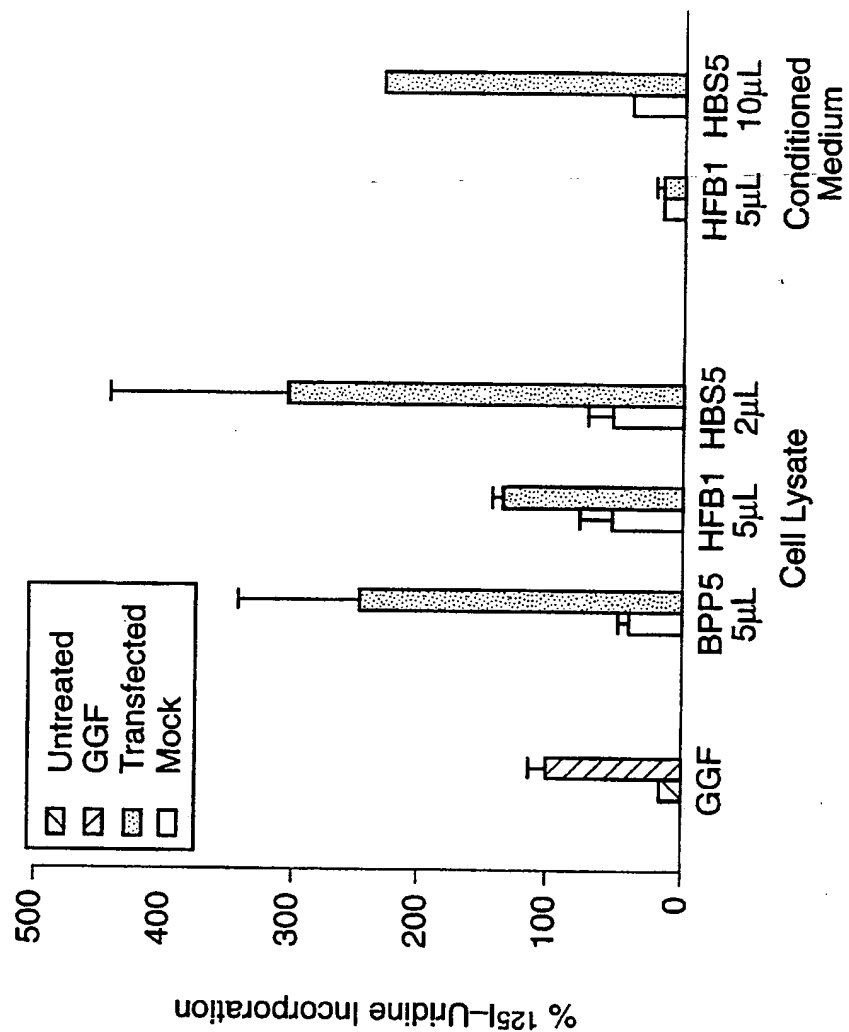


FIG. 47

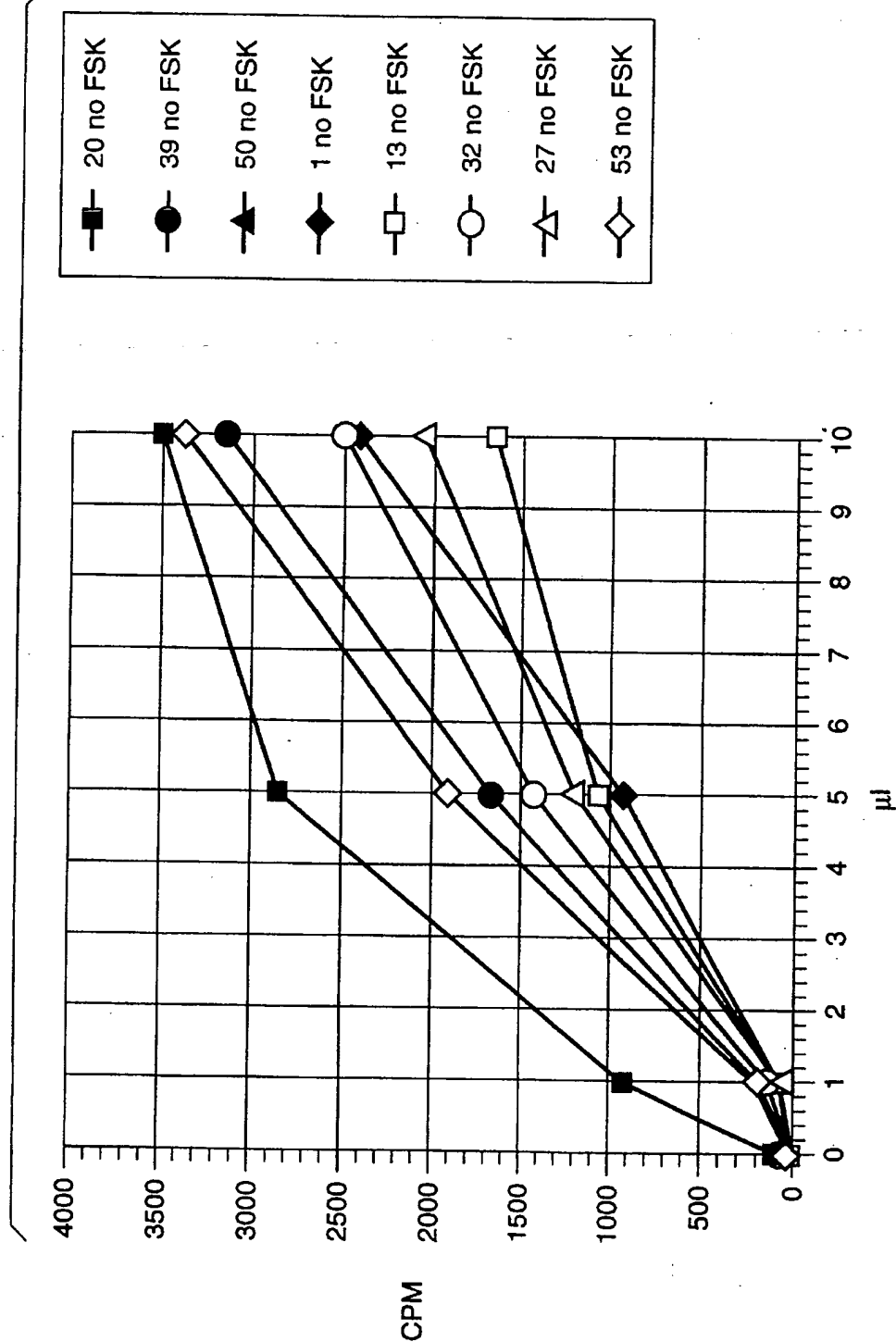


FIG. 48
Schwann Cell Assay/Baculovirus Clones

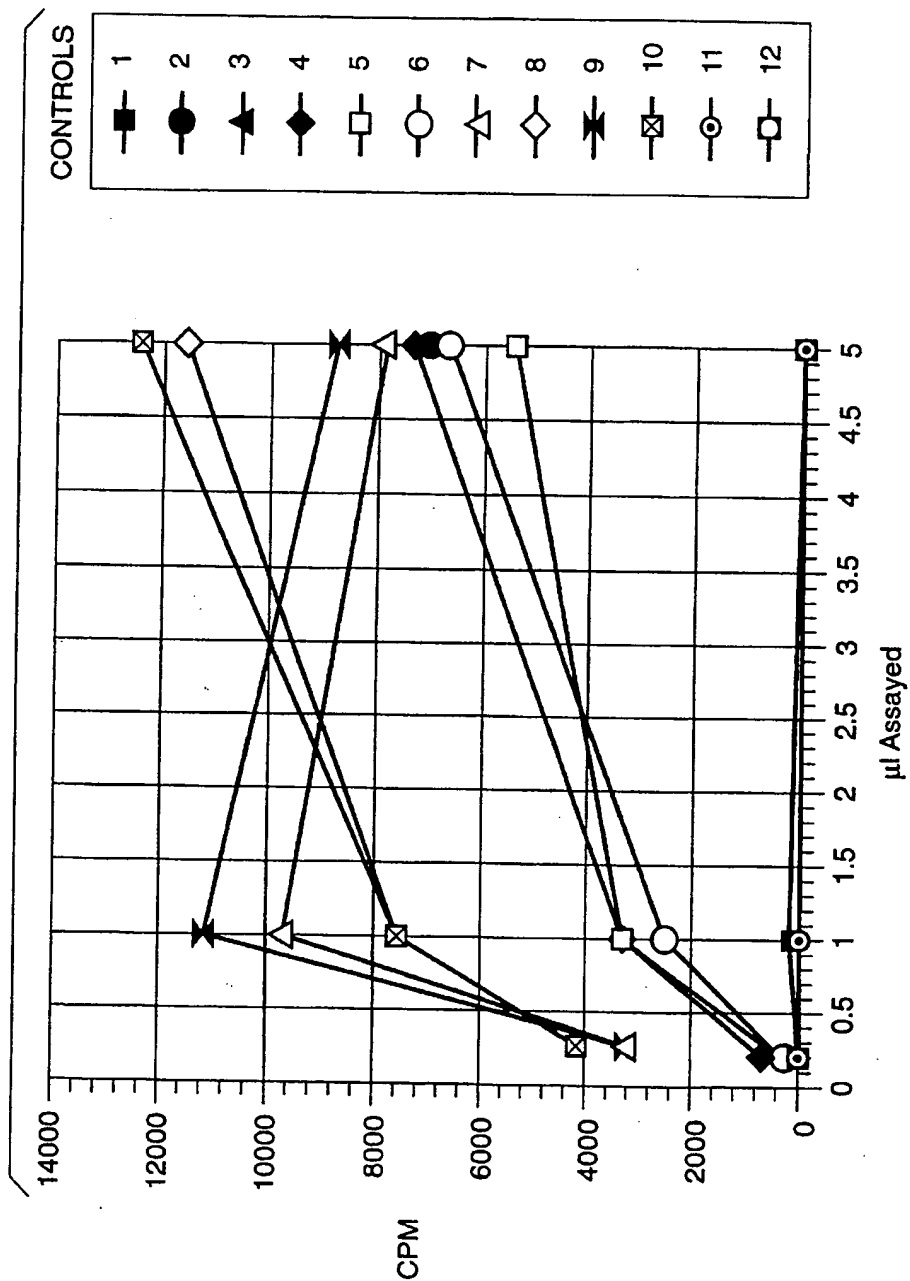


FIG. 49

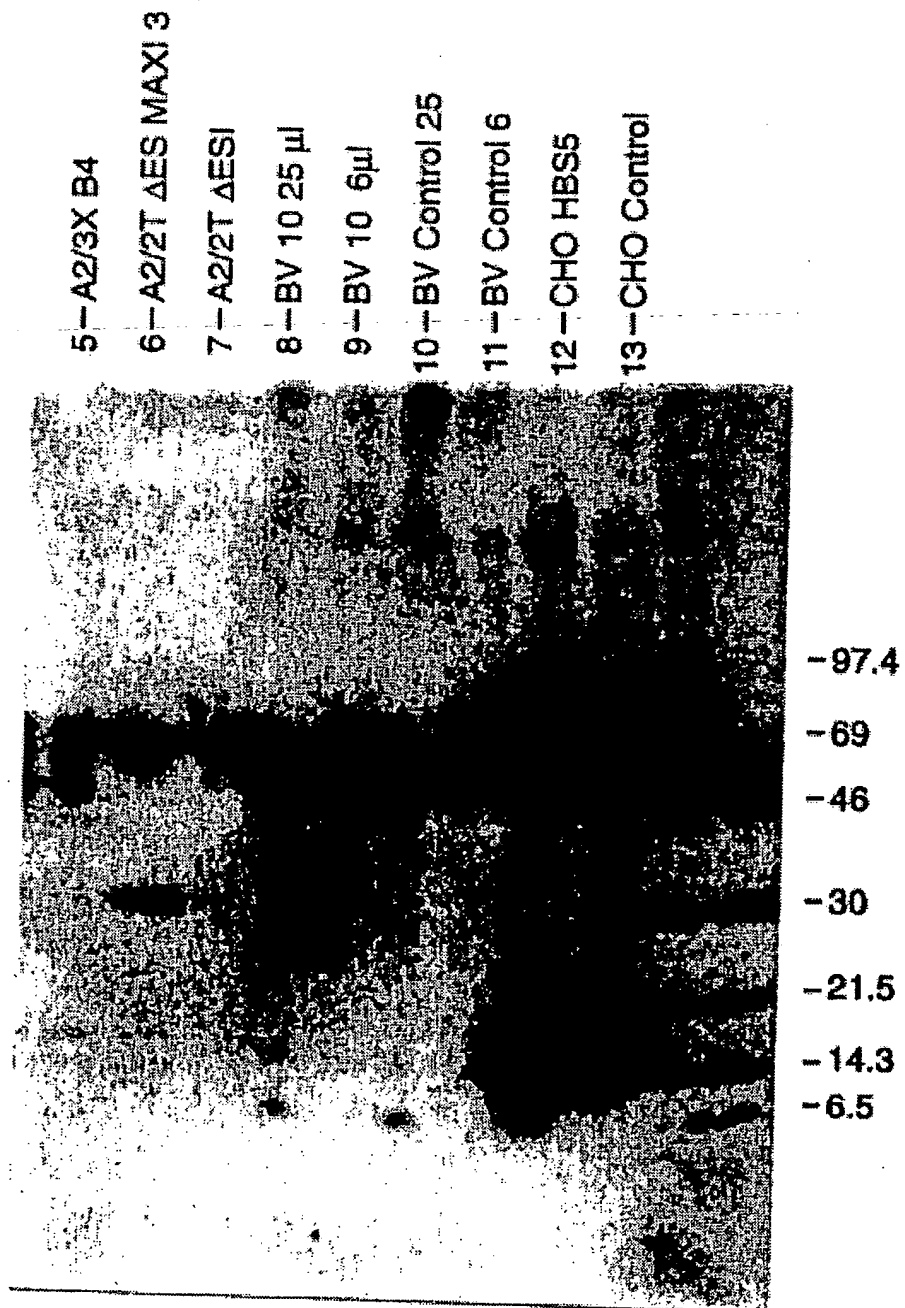


FIG. 50A

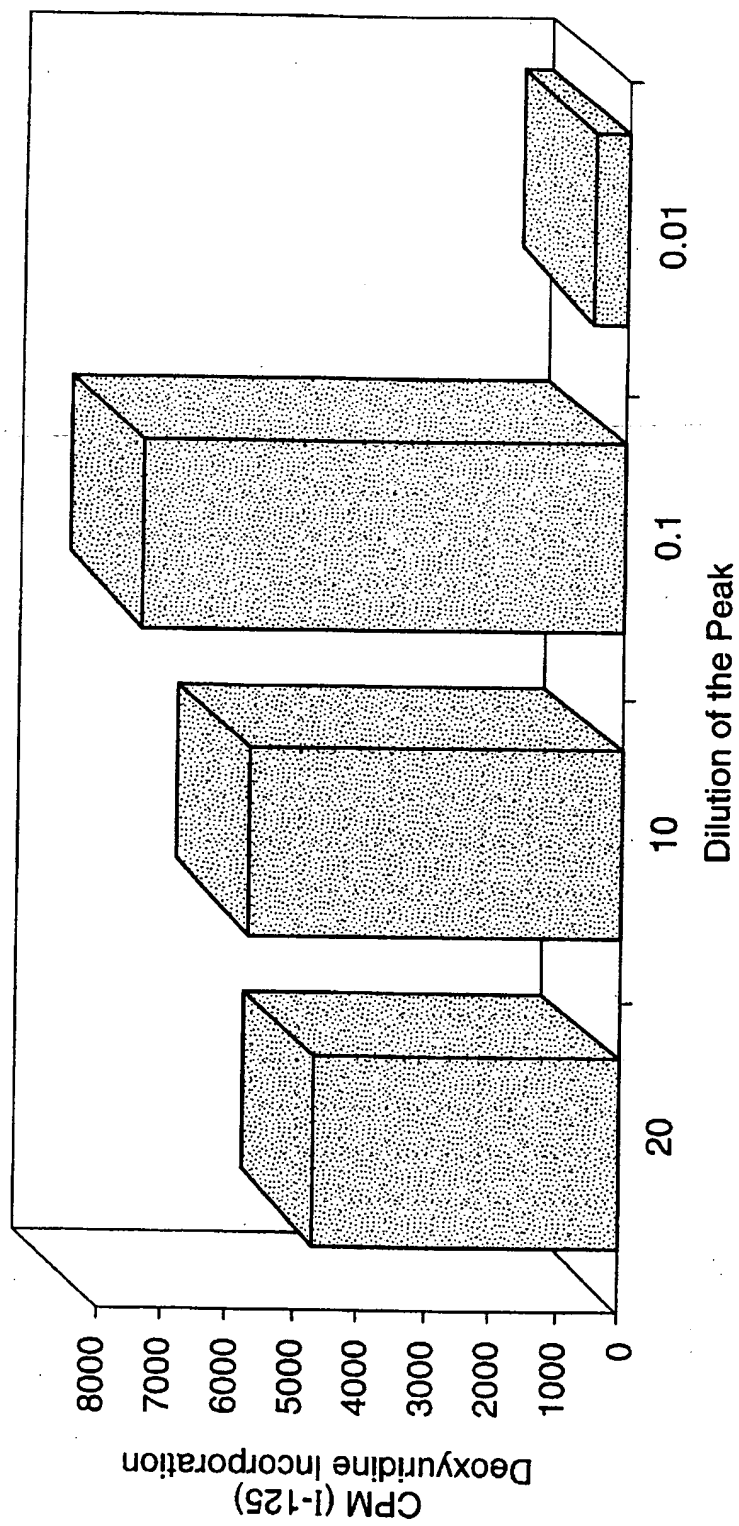


FIG. 50B

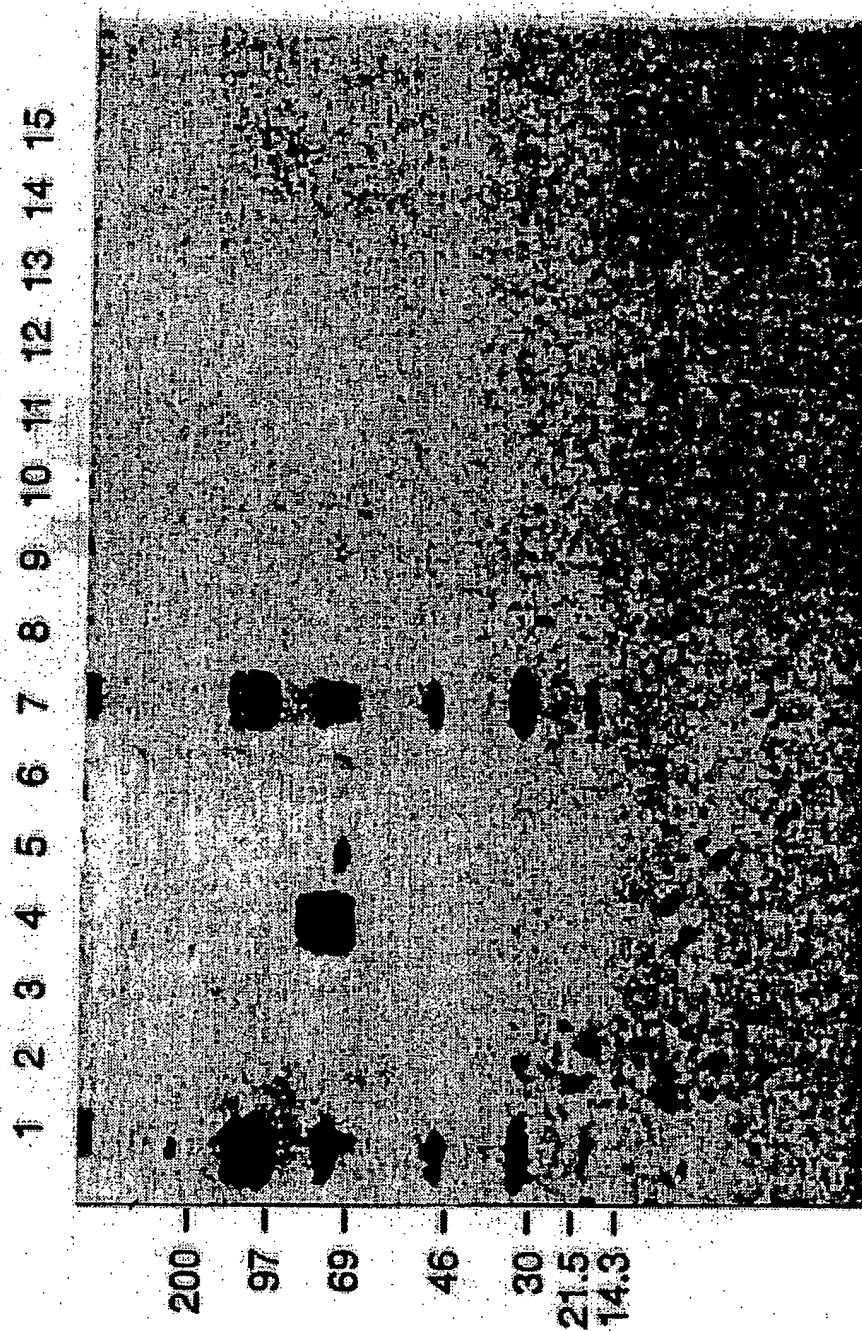


FIG. 51
rGGF Purification on Cation Exchange Column

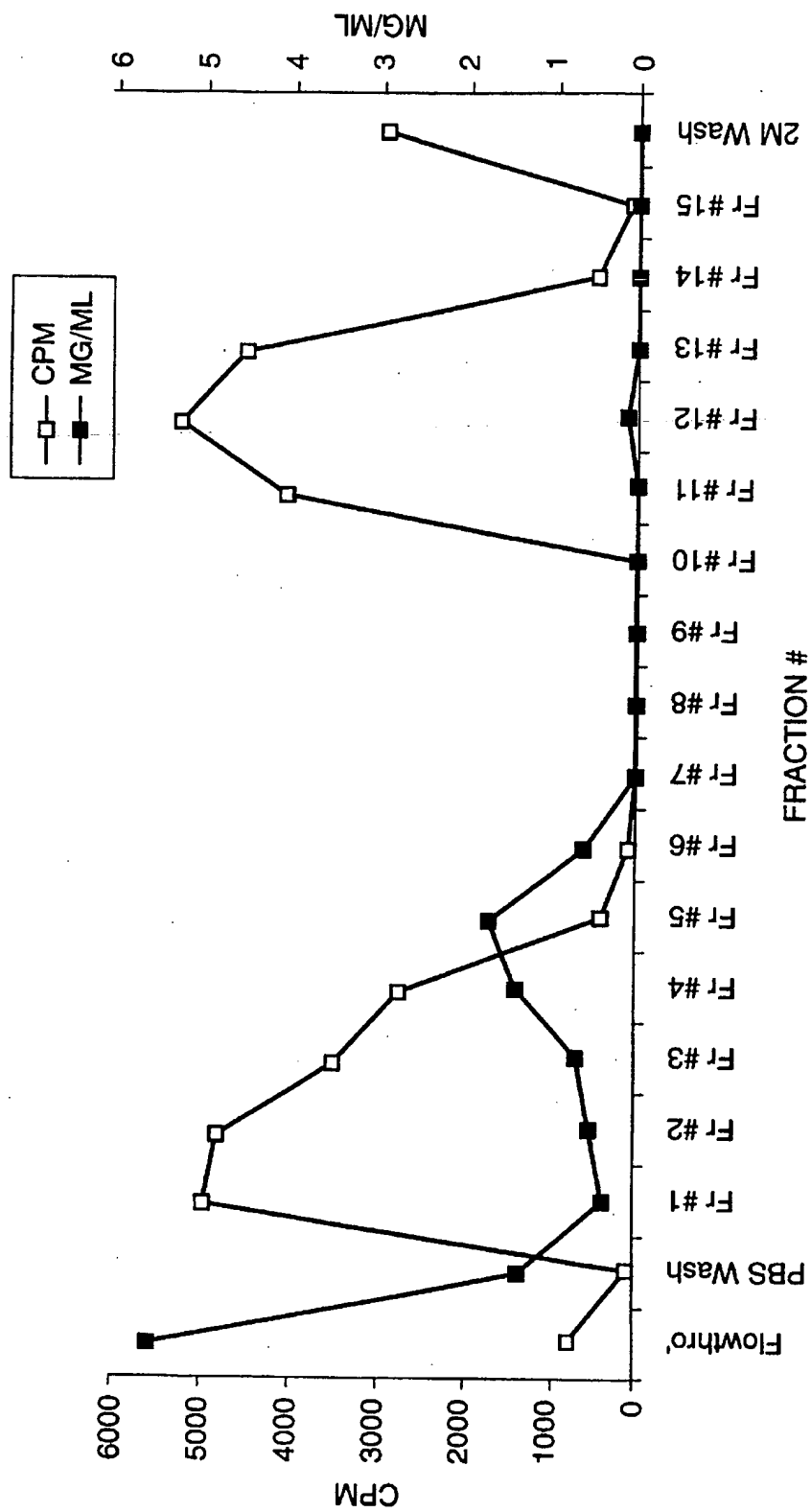


FIG. 51A

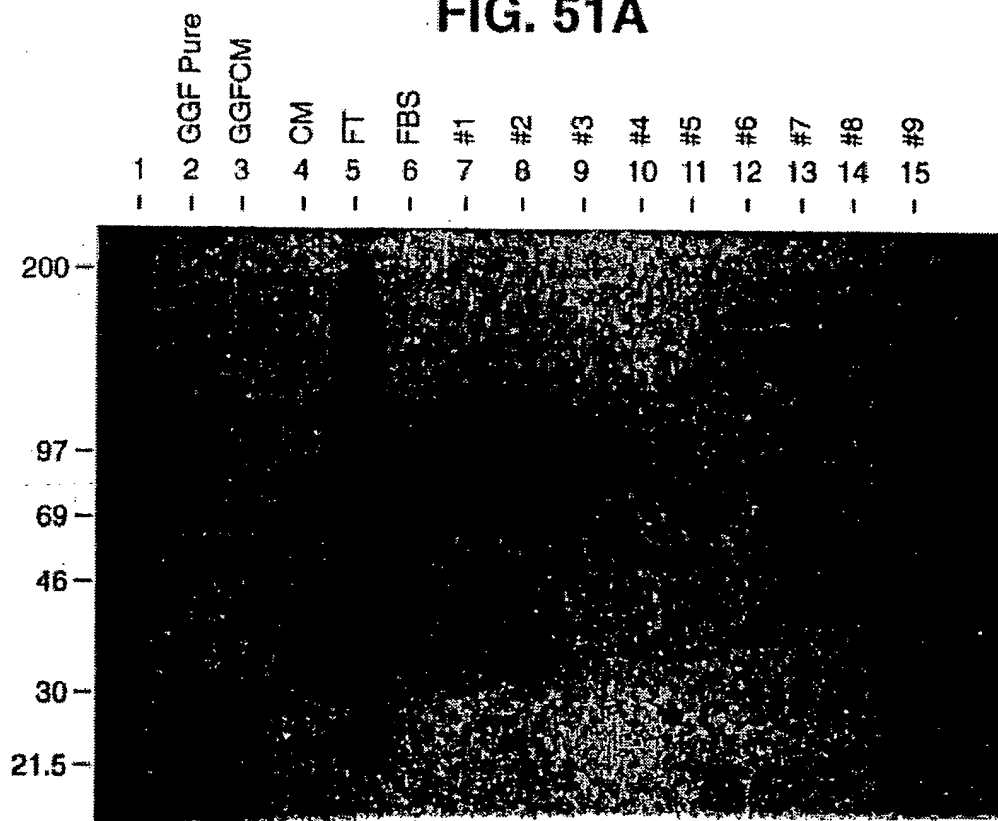


FIG. 51B

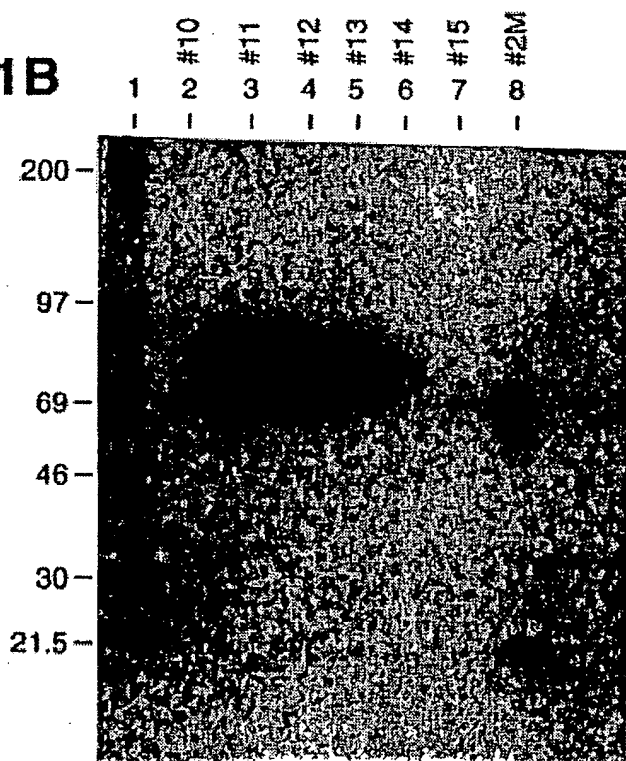
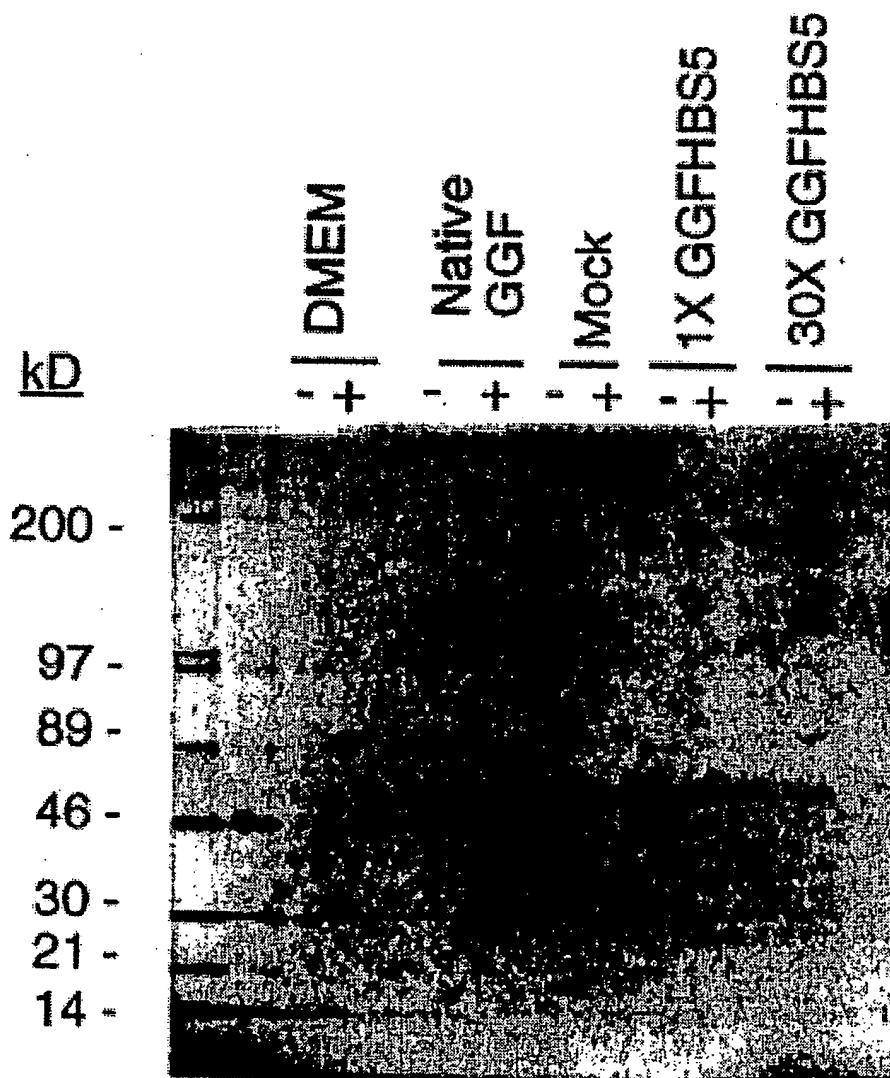


FIG. 52



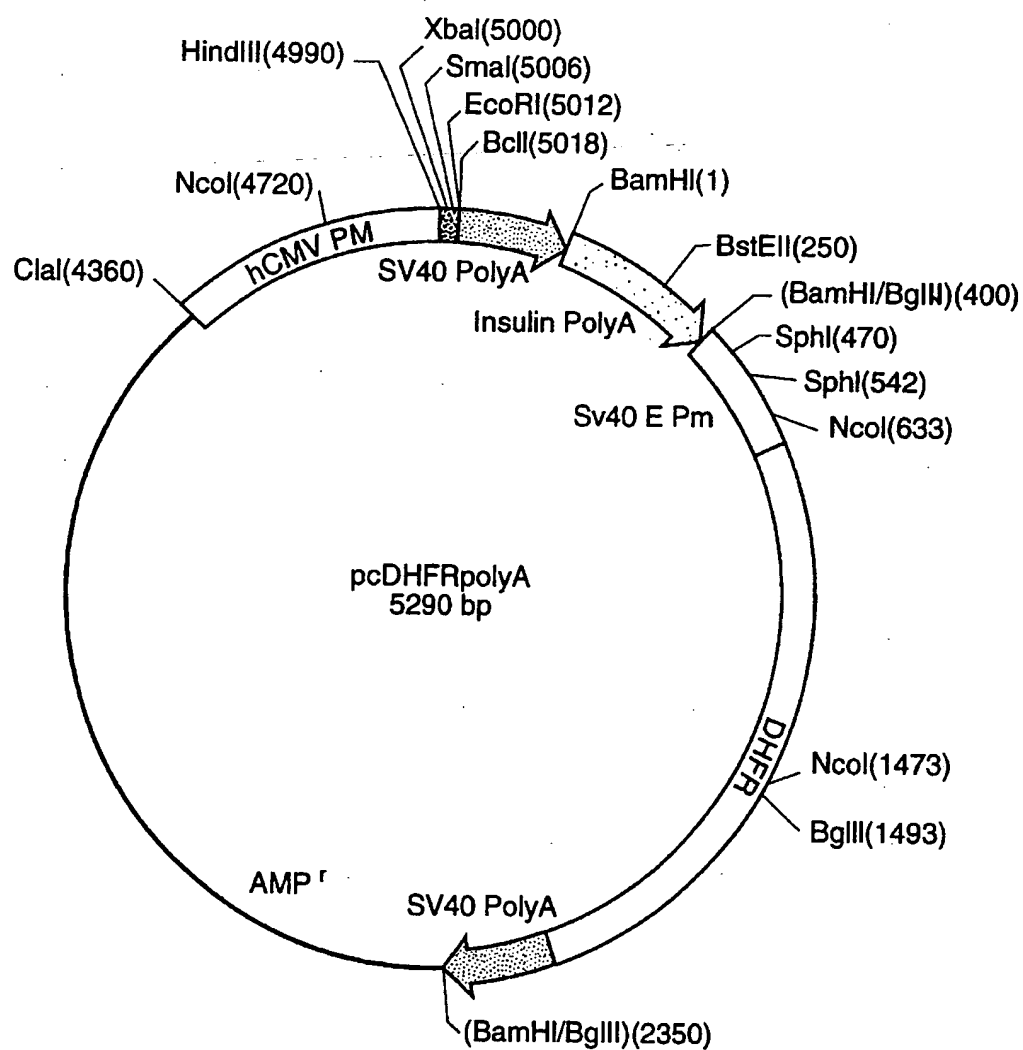
| | | | | |
|----------------|---------|---|---|--|
| SEQ ID NO:170 | GGFHBS5 | 1 | 1 | MRMRAPRRSGRPGPRAQRPGSAARSSPPLPLPLLLLTAAALAPCAAAAGNEAAPAGAS |
| | | | II-8 | II-4 |
| 61 | | | VCYSSPPSVGSVQELAQRAAVVIEGKVHPQRRQQGALDRKAAAAAGEAGAWGGDREPPAA | |
| | | | II-1 | II-10 |
| 121 | | | GPRALGPAAEPLLAANGTVPSWPTAPVPSAGEPGEAPYLKVHVQVAVKAGGLKKDSL | |
| | | | II-3 | II-2 |
| 181 | | | LTVRLGTWGHPAFPSCGRLKEDSRVYFFMEPDANSTSRAPAAFRASFPFPLETGRNLKKEV | |
| | | | 3 | |
| GGFHBS5 | 241 | | SRVLCRC | |
| SEQ ID NO: 171 | GGFHFB1 | 1 | O | OMSERKEGRGKGKGGKRGSGKKPESAAAGSQSP |
| SEQ ID NO: 172 | GGFBPP5 | 1 | R | K |
| | | | II-14 | II-11 |
| 268 | | | II-18 | I-7, II-12, |
| 53 | | | | III-13 |
| 53 | | | LVLRCETSSEYSSLRFKNFKNGNELNRKNKPQNIQKKPGKSELRKASLADSGEYMC | |
| | | | 4 | II-12 |
| 328 | | | K | S |
| 113 | | | II-12 | 5 |
| 113 | | | KVISKLGNDSASANITIVESN | |
| | | | EIITGMPASTEAGAYVSSSESPIRISVTEGANTSSS | |
| | | | 6 | II-15 |
| 354 | | | TTGTSHLVKCAEKEKTFVNGGECFVMVKDLSNPSRYLCKCPNEFTGDRCONVVMASFYST | |
| 173 | | | A | |
| 173 | | | | |
| | | | 9 | |
| 413 | | | STPFLSLPE* | |
| 232 | | | | |
| 232 | | | | |

FIG. 53

Deduced Sequences
of Human & Bovine
Glial Growth Factors

FIG. 53
Deduced Sequences
of Human & Bovine
Gillal Growth Factors

FIG. 54



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